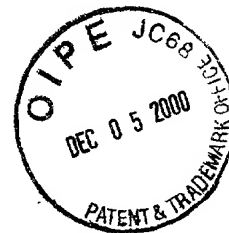


IN THE UNITED STATES PATENT & TRADEMARK OFFICE

In re application of)
)
Applicant: Gross et al.)
) Group Art Unit:
Title: Genes Coding for Tomato)
B-Galactosidase Polypeptides) Examiner:
)
International Application No.:)
PCT/US99/12697)
)
Docket No.: 0066.99)
)
International Filing Date: 6/8/99)



NATIONAL STAGE ENTRY

BOX PCT

Honorable Commissioner of Patents
And Trademarks
Washington, D.C. 20231

Sir:

The following documents and fees are submitted herewith in connection with the above application for the purpose of entering the National Stage under 35 U.S.C. §371 and in accordance with Chapter II of the Patent Cooperation Treaty:

- ☒ this express request to immediately begin national examination procedures [35 U.S.C. 371 (f)].
- ☒ an executed Declaration and Power of Attorney
- ☒ an English Language International Application with U.S. Search Report
- ☒ an executed Assignment w/ Assignment Recordation Coversheet

Docket No. 0066.99

- ☒ International Preliminary Examination Report
- ☒ Sequence Listing - Paper Readable and Computer Readable Copies

It is assumed that copies of the International Application, the International Search Report, the International Preliminary Examination Report, and any Article 19 and 34 amendments as required by §371(c) will be supplied directly by the International Bureau, but if further copies are needed, the undersigned can easily provide them upon request.

The Government filing fee is calculated as follows:

Total claims.....	<u>32</u>	- 20 =	<u>12</u>	x \$18 =	\$216.00
Independent Claims.....	<u>4</u>	- 3 =	<u>1</u>	x \$80 =	\$80.00
Base Fee.....	\$690.00				
TOTAL FILING FEE.....	\$986.00				

*A copy of the U.S. Search Report is attached.

Please charge these fees to deposit account 21-0561. The Commissioner is hereby authorized to charge any additional fees which may be required at anytime during the prosecution of this application, or credit any overpayment, to Deposit Account 21-0561.

Docket No. 0066.99

Priority is claimed from June 9, 1998, based on U.S.

Provisional Application No. 60/088,805.

Respectfully submitted,

December 5, 2000

Date

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09/701868

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IN THE UNITED STATES PATENT & TRADEMARK OFFICE

In re application of)
)
Applicant: Gross et al.)
) Group Art Unit:
Title: Genes Coding for Tomato)
B-Galactosidase Polypeptides) Examiner:
)
Serial No.: Unknown)
)
Docket No.: 0066.99)
)
Filed: Concurrently herewith)

Statement Pursuant to 37 C.F.R. 1.821 (f)

Sir:

Submitted for filing concurrently herewith in connection with the above-referenced patent application is a labeled, computer-readable copy of the Sequence Listing included with the application in accordance with 37 C.F.R. 1.821-1.824.

I hereby state that I have reviewed the paper copy of the Sequence Listing, as required by 37 C.F.R. 1.821 (c) and the computer readable form of the Sequence Listing, as required by 37 C.F.R. 1.821(e) and that the content of the paper and computer readable copies are the same.

Favorable consideration of the patent application is respectfully requested.

Respectfully submitted,

December 5, 2000
Date

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Enclosures:
Diskette
Sequence Listing

PATENT APPLICATION

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

In re application of)
)
Applicant: Gross et al.)
) Group Art Unit: 1646
Title: Genes Coding for Tomato)
B-Galactosidase Polypeptides) Examiner:
)
Serial No.: Unknown)
)
Docket No.: 0066.99)
)
Filed: Concurrently herewith)
)
)

SUBMISSION OF POWER OF ATTORNEY/DECLARATION AND ASSIGNMENT

Assistant Commissioner for Patents
Washington, D.C. 20231
ATTN: Application Branch

Sir:

Enclosed for filing in the above-identified application is a Declaration and Power of Attorney signed by all of the Applicants.

Also enclosed for filing is an Assignment document signed by all inventors and an Assignment Recordation Coversheet.

The Commissioner is hereby authorized to charge any additional fees which may be required at anytime during the

Docket No. 0066.99

prosecution of this application, or credit any overpayment, to
Deposit Account 21-0561.

Respectfully submitted,

December 5, 2000
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Declaration
Assignment Recordation Coversheet
Assignment

cc:
K. Gross
D. Smith

GENES CODING FOR TOMATO β -GALACTOSIDASE**POLYPEPTIDES**

5

Field of the Invention

The present invention relates to a family of novel plant genes encoding polypeptides characterized by their ability to hydrolyze terminal non-reducing β -D-galactosyl residues from β -D-galactosides. More specifically, a polynucleotide sequence derived from a cDNA clone designated pZBG2-1-4 (referred to in U.S. Provisional Appln. No. 60/088,805 as pTom β gal 4), which encodes a specific plant polypeptide named β -galactosidase II, is provided. Also provided are cDNA clones encoding six other homologous polypeptides, methods of using these cDNA clones for producing β -D-galactoside polypeptides of the invention, and methods of modifying fruit quality by employment of a polynucleotide or polypeptide of the present invention.

Background of the Invention

The most conspicuous and important processes related to post-harvest quality of climacteric fruit are the changes in texture, color, taste, and aroma which occur during ripening. Because of the critical relationship that deleterious changes in texture have to quality and post-harvest shelf-life, emphasis has been placed on studying the mechanisms involved in the loss of firmness that occurs during tomato fruit ripening. Although fruit softening may involve changes in turgor pressure, anatomical characteristics and cell

wall integrity, it is generally assumed that cell wall disassembly leading to a loss of wall integrity is a critical feature. The most apparent changes, in terms of composition and size, occur in the pectic fraction of the cell wall (see references in Seymour and Gross, 1996).

5 Changes known to occur in the pectic fraction of the cell wall during fruit ripening include increased solubility, depolymerization, de-esterification and a significant net loss of neutral sugar containing side chains (Huber, 1983; Fischer and Bennett, 1991; Seymour and Gross, 1996). The best characterized pectin-modifying enzymes are polygalacturonase (endo- α 1 \rightarrow 4-D-galacturonan
10 hydrolase; E.C. 3.2.1.15; PG) and pectin methylesterase (E.C. 3.1.1.11; PME). Although PG and PME are relatively abundant and have substantial activity during tomato fruit ripening, softening still occurs, albeit with a slight delay, in fruit where PG (Smith *et al.* 1988, 1990) or PME (Tieman *et al.* 1992; Hall *et al.* 1993) gene expression and enzyme activity was significantly down-
15 regulated in transgenic plants. Moreover, over-expression of PG in non-ripening mutant *rin* tomato fruit did not result in softening even though depolymerization and solubilization of pectin was evident (Giovannoni *et al.*, 1989).

 Among the other known pectin modifications that occur during fruit
20 development, one of the best characterized is the significant net loss of galactosyl residues which occurs in the cell walls of many ripening fruit (Gross and Sams, 1984; Seymour and Gross, 1996). Although some loss of galactosyl residues could result indirectly from the action of PG, β -galactosidase (exo- β (1 \rightarrow 4)-D-galactopyranoside; E.C. 3.2.1.23) is the only enzyme identified in

higher plants capable of directly cleaving $\beta(1\rightarrow4)$ galactan bonds, and probably plays a role in galactan sidechain loss (DeVeau *et al.*, 1993; Carey *et al.*, 1995; Carrington and Pressey, 1996). No endo-acting galactanase has yet been identified in higher plants. The view that β -galactosidase is active in releasing galactosyl residues from the cell wall during ripening is supported by the dramatic increase in free galactose, a product of β -galactosidase activity (Gross, 1984) and a concomitant increase in activity of a particular enzyme, designated β -galactosidase II, in tomatoes during ripening (Carey *et al.*, 1995). β -galactosidase activity is thought to be important in cell wall metabolism (Carey *et al.*, 1995). β -Galactosidases are generally assayed using artificial substrates such as *p*-nitrophenyl- β -D-galactopyranoside (PNP), 4-methylumbelliferyl- β -D-galactopyranoside and 5-bromo-4-chloro-3-indoxyl- β -D-galactopyranoside (X-GAL). However, it is clear that β -galactosidase II is also active against natural substrates, *i.e.*, $\beta(1\rightarrow4)$ galactan (Carey *et al.*, 1995; Carrington and Pressey, 1996; Pressey, 1983). β -Galactosidase proteins have been purified and characterized in a number of other fruits including kiwifruits (Ross *et al.*, 1993), coffee (Golden *et al.*, 1993), persimmon (Kang *et al.*, 1994), and apple (Ross *et al.*, 1994).

Carey *et al.* (1995) were able to purify three previously identified β -galactosidases from ripening tomato fruit (Pressey, 1983), but only one (β -galactosidase II) was active against $\beta(1\rightarrow4)$ galactan. Even though they were able to identify putative β -galactosidase cDNA clones, none of the cDNA's deduced amino acid sequences matched the amino terminal sequence of the β -galactosidase II protein. Although β -galactosidase II, a protein present in

tomato (*Lycopersicon esculentum* Mill.) fruit during ripening and capable of degrading tomato fruit galactan has been purified, cloning of the corresponding gene has been elusive.

The modification of plant gene expression has been achieved by several methods. The molecular biologist can choose from a range of known methods to decrease or increase gene expression or to alter the spatial or temporal expression of a particular gene. For example, the expression of either specific antisense RNA or partial (truncated) sense RNA has been utilized to reduce the expression of various target genes in plants (as reviewed by Bird and Ray, 1991, Biotechnology and Genetic-Engineering Reviews 9:207-227). These techniques involve the incorporation into the genome of the plant of a synthetic gene designed to express either antisense or sense RNA. They have been successfully used to down-regulate the expression of a range of individual genes involved in the development and ripening of tomato fruit (Gray et al, 1992, Plant Molecular Biology, 19:69-87). Methods to increase the expression of a target gene have also been developed. For example, additional genes designed to express RNA containing the complete coding region of the target gene may be incorporated into the genome of the plant to "over-express" the gene product. Various other methods to modify gene expression are known; for example, the use of alternative regulatory sequences. The complete disclosure of each of the references cited above is fully incorporated herein by reference.

The need therefore exists to clone a gene for β -galactosidase II and related polypeptides, and using known methods of modification of plant gene expression, thereby to provide methods for modifying quality of fruits,

particularly by modifying the cell wall, thereby directly affecting the ripening of the fruit.

Summary of the Invention

5 The present invention is based on the discovery of novel DNA sequences derived from cDNA clones from a family of genes encoding β -galactosidases. The phylogenic tree based on the shared amino acid sequence identities for the DNA sequences of the present invention is shown in Figure 1A,B. Five cDNA and two RT-PCR clones, designated herein as TBG1, TBG2, TBG3, TBG4,
10 TBG5, TBG6, and TBG7 and having the nucleic acid sequences designated SEQ ID NOs 1-7, respectively as shown in Figure 2, were identified which had a high degree of shared sequence identity to other known β -galactosidases. The corresponding amino acid sequences are designated herein as SEQ ID NOs 8-16, respectively and are shown in Figure 2 and 3. The nucleotide
15 sequences for SEQ ID NOs 1-7 are recorded in Gen Bank with the following respective Accessions Numbers:

SEQ ID NO:1	TGB1	AF023847	deposit Sept 10, 1997
SEQ ID NO:2	TGB2	AF154420	deposited May 19, 1999
SEQ ID NO: 3	TGB3	AF154421	deposited May 20, 1999
20 SEQ ID NO:4	TGB4	AF020390	deposited Aug 21, 1997
SEQ ID NO:5	TGB5	AF154423	deposited May 20, 1999
SEQ ID NO:6	TGB6	AF154424	deposited May 20, 1999
SEQ ID NO: 7	TGB7	AF154422	deposited May 20, 1999

Throughout the following discussion, wherever TBG4 is indicated in the description of the invention, it is to be understood that TBG1-3 and 5-7 are also to be included in that description, unless otherwise indicated.

5 A method of providing a DNA sequence of the invention, either by cloning a cDNA (for instance, pZBG2-1-4) that codes for a protein of the present invention, such as β -galactosidase II, or by deriving the DNA sequence from genomic DNA, or by synthesis of a DNA sequence ab initio using the cDNA sequence as a guide is also provided.

10 A method for modifying cell wall metabolism which involves modifying the activity of at least one galactosidase, and thus modifying the quality of the fruit is also provided.

Also provided by the present invention is a DNA construct including some or all of an exemplary β -galactosidase DNA sequence under control of a transcriptional initiation region operative in plants, so that the construct can
15 generate RNA in plant cells.

Also discovered is an enhancer/promoter associated with expression of the genes encoding β -galactosidase.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells
20 containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of β -galactosidase polypeptides or peptides by recombinant techniques.

The present invention also provides plant cells containing DNA constructs of the present invention; plants derived therefrom having modified β -galactosidase gene expression; and seeds produced from such plants.

5 The β -galactosidase II protein of the present invention has demonstrated enzyme activity in cell wall disassembly leading to loss of tissue integrity and fruit softening. The β -galactosidase II protein also may be involved in cell wall turnover, which could be involved in cell extension and/or expansion and therefore plant growth and development.

10 By hydrolyzing galactose from the cell wall, the enzyme may allow ripening to commence and/or progress, since galactose may be involved in stimulating ethylene production alone or in conjunction with unconjugated N-glycans.

15 The β -galactosidase of the invention may be involved in conversion of chloroplasts (green – chlorophyll) to chromoplasts (red – lycopene) during fruit ripening by degrading chloroplast membrane galactolipids.

The family of genes represented by the nucleotide sequences shown in Figure 2 is expected to code for a group of similar enzymes with the same type of hydrolytic activity but with different tissue and/or substrate specificity's or cellular compartmentation profiles.

20 The β -galactosidase II protein of the present invention as well as other proteins encoded in the nucleotide sequences shown in Figure 2 may be used for preparation of pectin and other cell wall derived polymers with lowered galactosyl content for use in biofilms and solutions (for example in

clarification of fruit juices) requiring lower or higher cross-linking or viscomertric properties.

The present invention also provides β -galactosidase enzymes for use as components of enzyme mixtures for protoplast isolation.

Brief Description of the Figures

Figure 1A and 1B shows a phylogenic tree based on shared amino acid sequence identity among tomato β -galactosidase clones TGB1-7 and other known plant β -galactosidase polypeptides.

Figure 2 shows cDNA sequences [SEQ ID NOs: 1-7, respectively] for the seven β -galactosidase genes of the invention: TGB1, TGB2, TGB3, TGB4, TGB5, TGB6, TGB7.

Figure 3 shows multiple sequence alignment of the deduced amino acid sequences of tomato fruit for cDNA clones TGB1, TGB2, TGB3, TGB4, TGB5, TGB6 and TGB7 [SEQ ID NOs: 8-16, respectively] and various plant β -galactosidase cDNA clones.

Figure 4 shows autoradiograph of northern blot analysis of TBG expression in various plant tissues (flowers, leaves, roots and stems).

Figure 5 shows Autoradiograph of northern blot analysis of TBG expression in fruit tissues at different stages of development.

Figure 6 shows autoradiograph of northern blot analysis of TBG expression in fruit tissues (mature green or turning stage fruit peel, outer pericarp, inner paricarp and locular).

5 **Figure 7** shows autoradiograph of northern blot analysis of TBG expression in normal and mutant fruit tissues.

Figure 8 shows autoradiograph of northern blot analysis of TBG expression in response to ethylene treatment of mature green fruit tissues.

10

Figure 9 shows Western blot analysis of TBG4 expression by yeast.

Figure 10 shows detection of β -galactosidase activity from pZBG2-1-4 expression in *E. coli*.

15

Figure 11 A - E (1-4) shows the comparative results of texture measurements for fruit from tomato plants containing antisense constructs to suppress TBG4 mRNA and fruit from the parental line.

20

Figures 12A - B show Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct.

Figure 13 shows a Binary construct used to transform plants and express TBG4 (pZBG2-1-4) in the antisense orientation.

25

Detailed Description

The following detailed description is directed to a preferred embodiment of the present invention and is intended as illustrative of each of other DNA sequences of the present invention.

5 The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding β -galactosidase polypeptides, particularly a β -galactosidase II polypeptide having the amino acid sequence shown in Figure 2. The DNA sequence of the exemplary β -galactosidase II cDNA clone of the invention, which was determined from a cDNA clone,
10 pZBG2-1-4, encoding β -galactosidase II, is recorded in GenBank as Accession Number AF020390. Not all β -galactosidases possess *in vitro* activity against extracted cell wall material via the release of galactose from wall polymers containing $\beta(1\rightarrow4)$ -D-galactan. The polypeptide expressed from the exemplary β -galactosidase II clone, pZBG2-1-4, has been shown to exhibit
15 β -galactosidase activity and exogalactinase activity.

 The exemplary β -galactosidase II protein of the present invention, as shown in Figure 2, shares sequence homology with the amino acid sequence deduced from β -galactosidase cDNA clones of TBG2-7 and cDNA clones of the fruits of asparagus (accession number P45582), apple (accession number
20 P48981), and carnation (accession number Q00662), as well as with β -galactosidase cDNA clones of a previously published sequence of a tomato β -galactosidase cDNA clone designated pTom β gal1 (accession number P48980) isolated from ripe 'Ailsa Craig' fruit (Carey *et al.*, 1995). The ORF of the clone TBG1 disclosed herein by the inventors (accession number AF023847)

is nearly identical to the cDNA previously described by Carey et al. As shown in Figure 2, the shared deduced sequence identity is high among all the published plant β -galactosidases of the seven clones (TBG1-7) and the other plant β -galactosidases.

5 BLAST searches of the database also indicated significant shared sequence identity between domains of the plant β -galactosidases and mammalian and fungal β -galactosidases, however little share sequence identity was detected with bacterial β -galactosidases.

10 As shown in Figure 1, the shared amino acid identity of TBG1 and TBG3 was high. TBG4 was also very similar to both TBG1 and 3. The amino acid sequences of TBG2 and 7 were unique because several regions of amino acid insertions appear throughout their sequence (Figure 3).

Nucleic Acid Molecules

15 Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using a PCR-based dideoxynucleotide terminator protocol and an ABI automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, CA), and all amino acid sequences of polypeptides encoded by DNA molecules
20 determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least

about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

By "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U).

Using the information provided herein, such as the exemplary nucleotide sequence shown in Figure 2 [SEQ ID NO: 4], a nucleic acid molecule of the present invention encoding a β -galactosidase II polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Illustrative of the invention, the nucleic acid molecule described in Figure 2 [SEQ ID NO: 4] was discovered in a cDNA library derived from breaker, turning and pink fruit pericarp from 'Rutgers' tomato plants.

The complete sequence of the cDNA insert of pZBG2-1-4 is accessible in the GenBank (no. AF020390) and is provided in Figure 2 [SEQ ID NO: 4].

The cDNA insert is 2532 nucleotides (nt) long and contains a single, long open reading frame (ORF) predicted to start with the first in-frame ATG at nt 64

5 and end with TAA at nt 2238. This ORF codes for a 79 kD protein 724 amino acids long. The deduced amino acid sequence of pZBG2-1-4 shared

significant amino acid identity to all published plant β -galactosidase sequences in the database (Figure 1A,B). When the entire ORF of each β -galactosidase

gene was compared to pZBG2-1-4, the shared sequence identity was about

10 64% for tomato pTom β gal 1 (P48980), about 67.6% for apple (P48981), about 63% for asparagus (P45582) and about 55% for carnation (Q00662). As one

of ordinary skill would appreciate, due to the possibilities of sequencing errors discussed above, the actual complete β -galactosidase II polypeptide encoded

by the deposited cDNA, which comprises about 724 amino acids, may be

15 somewhat longer or shorter. More generally, the actual open reading frame

may be anywhere in the range of ± 20 amino acids, more likely in the range of

± 10 amino acids, of that predicted from either the first methionine codon from

the N-terminus shown in Figure 2 [SEQ ID NO: 4]. In any event, as discussed

further below, the invention further provides polypeptides having various

20 residues deleted from the N-terminus of the complete polypeptide, including

polypeptides lacking one or more amino acids from the N-terminus of the β -

galactosidase II polypeptide described herein.

Leader and Mature Sequences

Analysis of the deduced amino acid sequence of pZBG2-1-4 suggested a high probability for secretion based on the presence of a hydrophobic leader sequence, a leader sequence cleavage site and three possible N-glycosylation sites. The programs PSORT V6.4 (Nakai and Kanehisa, 1992, incorporated herein by reference) and SignalP V1.1 (Nielsen et al., 1997, incorporated herein by reference), were used to predict that the ORF contains a hydrophobic leader sequence that would be cleaved between the alanine and serine residues at positions 23 and 24 respectively, and that the mature polypeptide has an extracellular location. The mature polypeptide contains three possible N-glycosylation sites at asparagine numbers 282, 459 and 713, however the asparagine at position 713 is unlikely to be glycosylated due to the proline at position 714. The predicted molecular mass of the unglycosylated mature polypeptide was 75 kD with a pI of 8.9.

Accordingly, the amino acid sequence of the complete β -galactosidase II protein of the invention includes a leader sequence and a mature protein, as shown in Figure 3 [SEQ ID NO: 4]. More in particular, the present invention provides nucleic acid molecules encoding a mature form of the β -galactosidase II protein. Thus, according to the signal hypothesis, secreted proteins have a signal or secretory leader sequence which is cleaved from the complete polypeptide to produce a secreted "mature" form of the protein. In some cases, cleavage of a secreted protein is not entirely uniform, which results in two or more mature species of the protein. Further, it has long been known that the cleavage specificity of a secreted protein is ultimately determined by the

primary structure of the complete protein, that is, it is inherent in the amino acid sequence of the polypeptide. Therefore, the present invention provides a nucleotide sequence encoding the mature β -galactosidase II polypeptide having the amino acid sequence encoded by the cDNA shown in Figure 2 [SEQ ID NO: 4] and provided in GenBank (Accession No. AF20390). By the “mature β -galactosidase II polypeptide having the amino acid sequence encoded by the cDNA clone shown in Figure 2 [SEQ ID NO: 4] is meant the mature form(s) of the β -galactosidase II protein produced by expression in a plant cell of the complete open reading frame encoded by the cDNA sequence of the clone shown in Figure 2 [SEQ ID NO: 4] and provided in GenBank (Accession No. AF20390).

The exemplary β -galactosidase II cDNA of the present invention (TBG4) has been expressed in *E. coli* strain XLI blue MR (lacZ) (Stratagene, La Jolla, CA), as described hereinbelow (see Example).

Analysis of the deduced amino acid sequence of cDNA clones representing the other β -galactosidase genes of the invention also revealed open reading frames and, in some cases, suggested a high probability for secretion of the encoded proteins. All the full-length cDNA clones were predicted to have a signal sequence (Fig. 2). Using the two prediction programs SignalP and PSORT, TBG4 was predicted to be secreted by both programs. TBG1, 2 and 3 were predicted to have cleavable signal sequences by SignalP, but uncleavable signal sequences by PSORT. TBG7 was suggested to be targeted to the chloroplast by PSORT. Particular observations for each of the seven clones are as follows, based on the presence of a hydrophobic

leader predicted by the programs PSORT V6. and SignalP V1.1: TBG1:
initiation codon at 306 [SEQ ID NO: 1], ORF = 835 amino acids [SEQ ID
NO: 8], signal sequence at 1-24; TBG2: initiation codon not determined [SEQ
ID NO: 2], ORF = 888 amino acids [SEQ ID NO: 9], signal sequence at 1-25;
5 TBG3: initiation codon at 32 [SEQ ID NO: 3], ORF = 838 amino acids [SEQ
ID NO: 10], signal sequence at 1-22; TBG5: initiation codon not determined
[SEQ ID NO: 5], ORF = 251 amino acids [SEQ ID NO: 12], signal sequence
not determined; TBG6: initiation codon not determined [SEQ ID NO: 6], ORF
= 248 amino acids [SEQ ID NO: 13], signal sequence not determined; TBG7:
10 initiation codon at 104 [SEQ ID NO: 7], ORF = 870 amino acids [SEQ ID
NO: 14], signal sequence at 1-35.

The deduced amino acid sequences of the seven clones was also
subjected to analysis using the program DNAsis and the predictions for
molecular mass, cellular targeting, pI and potential N-linked glycosylation
15 sites are summarized in Table I.

Table I. Tomato β -galactosidase (TBG) cDNA sequence data. Five full-length and 2 partial-length cDNAs were cloned and sequenced. The DNA and deduced amino acid sequence data is presented below

CLONE	mRNA(kb)	kD	pI	N-LINK	TARGET
TBG1	3.2	90.8	6.2	2	ER/OUT
TBG2	3.0	97.0	6.2	6	PM
TBG3	2.8	90.5	8.2	1	ER/OUT
TBG4	2.6	77.9	8.9	3	OUT
TBG5	~3				
TBG6	~3				
TBG7	3.0	93.3	8.0	6	CHLOR

N-LINK = possible N-linked glycosylation sites; ER = endoplasmic reticulum; out = secreted; PM = tethered to plasma membrane; CHLOR = chloroplast

As indicated, nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment

For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Isolated nucleic acid molecules of the present invention include DNA molecules comprising an open reading frame (ORF) with an initiation codon at position 64 of the nucleotide sequence shown in Figure 2 [SEQ ID NO: 4]. Also included are DNA molecules comprising the coding sequence for the mature β -galactosidase II protein shown at positions 135-2532 of Figure 2 [SEQ ID NO: 4].

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode the β -galactosidase II protein. Of course, the genetic code and species-specific codon preferences are well known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the plant mRNA to those preferred by a bacterial host such as *E. coli*). Preferably, this nucleic acid molecule will encode the mature polypeptide encoded by the above-described deposited cDNA clone.

The invention further provides an isolated nucleic acid molecule having the nucleotide sequence shown in Figure 2 [SEQ ID NO: 4] or a nucleic acid molecule having a sequence complementary to the above sequence. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping, by *in situ* hybridization with chromosomes, and for detecting expression of the β -galactosidase II gene in plant tissue, for instance, by Northern blot analysis.

The present invention is further directed to nucleic acid molecules encoding portions of the nucleotide sequences described herein as well as to fragments of the isolated nucleic acid molecules described herein. In particular, the invention provides a polynucleotide having a nucleotide sequence representing the portion of Figure 2 [SEQ ID NO: 4] which consists of positions 1-2538 of Figure 2 [SEQ ID NO: 4].

In addition, the invention provides additional nucleic acid molecules having nucleotide sequences related to extensive portions of Figure 2 [SEQ ID NO: 4] which have been determined from the following related cDNA clones: TBG1-3 and TBG5-7 as shown in Figure 3, SEQ. NO's 1-3 and 5-7

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, the cDNA clone shown in Figure 2 [SEQ ID NO: 4]. By "stringent hybridization conditions" is intended overnight incubation at 42° C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μ g/ml

denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65° C.

As indicated, nucleic acid molecules of the present invention which encode a β -galactosidase II polypeptide may include, but are not limited to those encoding the amino acid sequence of the mature polypeptide, by itself; and the coding sequence for the mature polypeptide and additional sequences, such as those encoding the about 1-23 amino acid leader sequence, such as a pre-, or pro- or prepro- protein sequence; the coding sequence of the mature polypeptide, with or without the aforementioned additional coding sequences.

Also discovered is an enhancer/promoter associated with expression of the genes encoding β -galactosidase. The inventors have characterized the expression profile of TBG2 mRNA and have cloned a lambda genomic cDNA. TBG2 is expressed before the onset of fruit ripening and continues at uniform level through all the ripening stages. TBG2 has been found to be expressed in all fruit tissues and has also been found to be fruit specific. Experiments have shown TBG2 to be unaffected by ethylene. TBG2 is expressed in the ripening mutants rin, nor and Nr at the normal chronological time after anthesis. The promoter discovered would be useful to express any gene in the sense or antisense orientation, specifically in tomato fruit, in all tomato fruit tissues, starting before and continuing throughout the entire ripening process. The promoter could also be used to express any gene in the ripening mutants rin, nor and Nr without the need to gas the fruit with exogenous ethylene.

Variant and Mutant Polynucleotides

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the β -galactosidase II protein. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the β -galactosidase II protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Most highly preferred are nucleic acid molecules encoding the mature protein having the amino acid sequence shown in Figure 2 as pZBG2-1-4 or the mature β -galactosidase II amino acid sequence encoded by the deposited cDNA clone.

Further embodiments include an isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 90%

identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to a polynucleotide selected from the group consisting of: (a) a nucleotide sequence encoding the β -galactosidase II polypeptide having the complete amino acid sequence in Figure 2 [SEQ ID NO: 4] (b) a nucleotide sequence
5 encoding the mature β -galactosidase II polypeptide shown in Figure 2 [SEQ ID NO: 4]; (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b) above.

Vectors and Host Cells

The present invention also relates to vectors which include the isolated
10 DNA molecules of the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of β -galactosidase II polypeptides or fragments thereof by recombinant techniques. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In
15 the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a
20 charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp*, *phoA* and *tac* promoters, the SV40 early and late promoters and promoters of

retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, StrepZBG2-1-4yces and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, 293 and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc., *supra*; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis *et al.*, *Basic Methods In Molecular Biology* (1986).

Example

Tomato (*Lycopersicon esculentum* Mill., cv. 'Rutgers') plants were grown in a greenhouse using standard cultural practices. The ripening mutants, *ripening inhibitor (rin)*, *non-ripening (nor)* and *never ripe (Nr)* (Tigchelaar *et al.*, 1978), were all in the 'Rutgers' background. Flowers were tagged at anthesis and fruit were harvested according to the number of days post-anthesis (dpa) or based on their surface color using ripeness stages as previously described (Mitcham *et al.*, 1989), the complete disclosure of which is hereby fully incorporated herein by reference. For gene expression studies, a variety of leaf, flower, and stem tissues were harvested from greenhouse-grown plants and roots were harvested from seedlings grown in basal tissue culture medium for 4 weeks after seed germination.

RNA Extraction

Fruits were processed immediately after harvest in the greenhouse by chilling on ice, excising the various tissues and freezing them in liquid nitrogen. Tissue samples were ground using a mortar and pestle and stored at -80°C. RNA was extracted using the method described in Verwoerd *et al.* (1989). Poly(A)RNA was purified from total RNA using oligo(dT) columns

(Pharmacia, Piscataway, NJ). RNA was quantified by measuring A_{260} using a dual beam spectrophotometer.

RT-PCR

5 Degenerate primers were designed based on the highest shared deduced amino acid sequence identity we found between an apple (accession number P48980), asparagus (P45582) and carnation (Q00662) β -galactosidase cDNA clones. The two primers used for the first reaction were BG5'E1 (WSNGGNWSNATHCAYTAYCC) and BG3'E (CCRTAYTCRTCNADNGGNGG). A second reaction was done on the products of the first reaction using BG5'I1 (ATHCARACNTAYGTNTTYTGG) and BG3'E. The degeneracy code for the primer sequences is N=a+t+c+g; H=a+t+c; B=t+c+g; D=a+t+g; V=a+c+g; R=a+g; Y=c+t; M=a+c; K=t+g; S=c+g; and W=a+t. The 5' and 3' primers 10 corresponded to amino acids 72-78 and 321-315 of the apple clone, respectively. Amplification was done using AmpliTaq DNA polymerase (Perkin Elmer, Norwalk, CT) and standard PCR conditions using the cDNA made for the first cDNA library described below as a template (Ausubel *et al.*, 1987). PCR products were separated in an agarose gel and fragments of the 15 expected size (approximately 750 bp) were purified, cloned into pCRscript (Stratagene, La Jolla, CA), and sequenced. 20

cDNA library

Two cDNA libraries were constructed. The first comprised poly(A) RNA 25 isolated from breaker, turning and pink fruit pericarp from 'Rutgers' plants.

The cDNA synthesis and library construction was done exactly according to the manufacturers instructions for the ZAP-cDNA Gigapack II Gold Cloning Kit (Stratagene), the complete disclosure of which is fully incorporated herein by reference. First-strand cDNA synthesis was primed using a poly(dT) primer and inserts were directionally cloned into the Uni-Zap XR vector using EcoRI and XhoI restriction sites. The second library comprised poly(A) RNA isolated from all fruit tissues (except seeds) from immature green, mature green, breaker, turning, pink, red-ripe and over-ripe fruit of 'Rutgers' plants.

The cDNA synthesis and library construction was done exactly according to the manufacturers instructions for the SuperScript Lambda System for cDNA synthesis and • Cloning (GibcoBRL, Gaithersburg, MD). First-strand cDNA synthesis was primed using a oligo(dT) primer and cDNA inserts were directionally cloned into the • ZipLox cloning vector using SalI and NotI restriction sites. Both libraries were amplified and maintained using the host strains provided by the manufacturer, according to their instructions.

One of the clones (RT-PCR2-1) was used to screen 10^6 plaques from the tomato fruit cDNA libraries at low stringency (hybridization at 45°C, no formamide and final wash with 0.2X SSC at 42°C). Thirty positive cDNA clones were identified and partially sequenced. Complete sequencing and characterization of the RT-PCR and cDNA clones revealed the possibility of seven unique β -galactosidase genes.

DNA and RNA Gel Blot Analysis

Southern analysis was done using the 3' UTR of each full length clone and the RT-PCR clones as probes against restriction enzyme digested genomic DNA. DNA gel blot analysis was done essentially as described in Smith and Fedoroff (1995) except that 3 µg of genomic DNA was used for each digest. The genes corresponding to the clones appeared to be present as single copies (data not shown). The same probes were used to map 6 of the 7 genes using RFLPs of recombinant inbred lines and the loci names and map positions are shown in Table II (James Giovannone, Texas A&M University, personal communication).

Table II. TBG loci map positions. Genes were mapped by Southern analysis using RFLPs of recombinant inbred lines.

Gene	chromosome	map position
TBG1	12*	overlap of IL 12-2, IL 12-3
TBG2	9	IL 9-3
TBG3	3	IL 3-5
TBG4	12*	overlap of IL 12-2, IL 12-3
TBG5	11	IL 11-3
TBG6	2	overlap of IL 2-4, IL 2-5
TBG7	no RFLP	

*TBG1 and 4 are loosely linked

Total RNA (20 µg/ lane) was separated in a formaldehyde/Mops agarose gel, transferred to Hybond-N⁺ nylon membrane (Amersham, Arlington Heights, IL), fixed by incubating for 2 h at 80°C, hybridized overnight in a

hybridization incubator (Robbins Scientific, Sunnyvale, CA) using a buffer described by Church and Gilbert (1984) washed to a final stringency of 0.1 X SSC with 0.2% SDS at 65°C, and autoradiographed essentially as described by Ausubel *et al.* (1987). An RNA ladder standard (GibcoBRL) was used to estimate the length of the RNAs. Probes were synthesized using a random priming kit with ³²P-dATP as the label (Boehringer Mannheim, Indianapolis, IN). Northern analysis was done using the 3' UTR of each full length clone and the RT-PCR clones as templates for probe synthesis. As a loading control, RNA blots were stripped and re-probed at a reduced hybridization and washing stringency using a soybean 26S rDNA fragment (Turano et al., 1997). For all hybridizations, ³²P(dATP)-labeled probe was diluted to 1-2 x 10⁶ dpm/mL. The complete disclosures of the above references are fully incorporated herein by reference.

Sequence Analysis

Sequencing was done at the Iowa State University Sequencing Facility (Ames, IA) using a PCR-based dideoxynucleotide terminator protocol and an ABI automated sequencer (Applied Biosystems, Foster City, CA). The sequencing of both cDNA insert strands was done by primer walking. Nucleotide and deduced amino acid sequence comparisons against the databases were done using BLAST searches (Altschul *et al.*, 1990). Sequence data were analyzed and aligned using DNA Strider 1.2 (Marck, 1988) and MacDNAsis (Hitachi, San Bruno, CA) software. The complete disclosures of the above references are fully incorporated herein by reference.

Northern Blot Analysis

Tissue Specific Expression

Northern blot analysis was done to reveal which, if any, of the β -galactosidase genes had a fruit-specific expression pattern. With the exception of TBG2, transcripts of all clones were detected in non-fruit tissues (Fig. 4). Transcripts of TBG 1, 4, 5 and 6 were detected in all the tissues tested. TBG3 transcript was detected at low levels in root and stem tissues, while TBG7 transcript was detected in flower and stem tissues.

Temporal expression pattern in fruit

The temporal expression pattern of the seven genes in fruit tissue was examined using RNA extracted from all fruit tissues except seeds. Transcripts for all seven genes were detected during some stage of fruit development (Fig. 5). TBG1 and 3 had similar expression patterns and their transcripts were detected throughout the breaker to over-ripe stages. TBG2 had a unique expression pattern and its transcript was detected at a constant level from 30 dpp to the over ripe stage. TBG4 expression pattern was similar to TBG1 and 3, but differed in that the transcript level was significantly higher at the turning stage. TBG5 had a similar expression pattern to TBG4 during the ripening stages of development, however TBG5 transcript was also detected throughout all the earlier stages of fruit development. TBG6 had an interesting expression pattern and its transcript was only detected at high levels in all pre-ripening stages tested. TBG7 also had a unique expression pattern and its transcript was detected at very low levels throughout all the stages tested, and at moderate levels at 10 dpp and the over-ripe stage.

Spatial expression pattern in fruit

Northern blot analysis was also done to determine transcript accumulation in various fruit tissues. Since there were temporal differences in the expression patterns of the TBG genes both the mature green and turning fruit stages were used for RNA extractions (Fig. 6). Both TBG2 and TBG6 transcripts were detected in all mature green fruit tissues tested. TBG7 transcript was present in all fruit tissues tested except for locules. Both TBG1 and TBG4 transcripts were detected in RNA samples extracted from all turning stage fruit tissues. TBG4 transcript was notably more abundant in the peel. TBG3 and TBG5 expression patterns were unique and their transcripts were detected in all tissues except the outer pericarp and locular respectively.

Expression in normal versus mutant fruit

In order to better understand the potential roles of the TBG products and transcriptional regulatory mechanisms, northern analysis was performed using fruit tissue from the ripening mutants *rin*, *nor* and *N'*. This analysis was important because it might give clues for preliminary determination of any potential ripening and/or softening role any of the TBGs might possess.

The results of mutant fruit Northern analysis suggested that the transcriptional regulation of TBG1, 2, 3, 5 and 7 was unaffected in mutant fruit tissue and that their transcripts were present in a normal chronological (dpp) pattern (Fig. 7). The abundance of TBG4 and 6 transcripts were however different in the mutant fruit. TBG4 transcript was not detected in fruit tissue of *N'* and was detected at much lower levels in *rin* and *nor* than wild type fruit

tissues. Normally TBG6 transcripts are detectable at high levels throughout the early stages of fruit development but are not detectable after the mature green stage (40-42 dpp). TBG6 transcripts persisted even to 50 dpp in fruit of all three mutants.

Transcriptional regulation by ethylene

The northern analysis done using mutant and wild type fruit suggested that TBG4 expression might be up-regulated by ethylene and that TBG6 expression might be down-regulated by ethylene. In order to evaluate this hypothesis mature green fruit were harvested and subjected to a continuous flow of 10 ppm ethylene mixed in air. Control and ethylene-treated fruit were used for RNA extractions at 1, 2, 12 and 24 hours. The results of this experiment confirmed the findings from the mutant fruit northern analysis. As expected, the presence and abundance of TBG1, 2, 3, 5 and 7 transcripts was essentially unaffected in mature green tissues subjected to exogenous ethylene treatment (Fig. 8). However, TBG4 transcript abundance was increased in mature green tissues in the presence of ethylene. From the data presented it was unclear whether TBG6 transcript abundance was reduced by exogenous ethylene treatment since its transcript level was normally reduced at this stage of fruit development.

Enzyme activity

In order to determine the role of the TBG encoded products we initiated experiments to express the cDNA encoded enzymes using heterologous expression systems. Several *E. coli* expression systems were

tested, but the yield of product was very low due to toxicity (See the example below). Therefore we used a yeast expression system which secretes a mature amino-terminal-FLAG fusion protein into the culture medium. The TBG4 cDNA was tested first and resulted in the production of approximately 1 mg

5 TBG4 active protein per 50 mls culture. TBG4 was used first because the cDNA codes for the enzyme β -galactosidase II which was purified from tomato fruit and has been characterized in some detail (Carey et al 1995, Smith et al 1998). Therefore we could compare the activity of the heterologous system-expressed protein to the native enzyme purified from tomato. The

10 TBG4 protein was successfully affinity purified using an anti-FLAG affinity resin (Figure 9).

The affinity-purified TBG4 enzyme was shown to have $\beta(1\rightarrow4)$ -D-galactosidase activity by virtue of its ability to hydrolyze the synthetic substrate p-nitrophenyl- β -D-galactopyranoside (Smith et al. 1998). The

15 enzyme can cleave galactosyl residues from a variety of cell wall substrates and therefore has exo-galactanase activity (Table III). The remaining full-length cDNA clones are currently being tested for successful expression of active enzyme. Preliminary results have shown that TBG1 codes for an enzyme which also has both β -D-galactosidase and exo-galactanase activity

20 (Table III).

Table III. Cell wall degrading activity of TBG4 and TBG1 expressed in yeast. Removal of galactosyl residues from chelator soluble (CSP) and alkali soluble (ASP) pectin and hemicellulosic (HCF) cell wall fractions purified from tomato fruit.

		μg galactose released	
enzyme	substrate	boiled	live
^a TBG4	CSP	0	5
	ASP	0	14.5
	HCF	0	4
^b TBG1	ASP	0	1.2

2 mg substrate; 4 hours at 37°C
^a.005 units enzyme/rx
^b.0005 units enzyme/rx

pZBG2-1-4 Codes for a β -Galactosidase

5 The TBG4 ORF was cloned in-frame into the repressible/inducible bacterial expression vector pFLAG-CTC. The host strain XL1-Blue MR is a mutant strain containing no endogenous β -galactosidase activity nor α -complementation. Induction of gene transcription by (IPTG) caused the immediate cessation of *E. coli* growth at 30 to 37°C. However, induction at 10 20°C did allow for some limited *E. coli* growth. When clones containing the pZBG2-1-4 4 ORF were grown at 20°C and induced with IPTG, the cells slowly turned blue after 36 hrs growth in medium containing the β -galactosidase substrate X-GAL, (Figure 10). If not induced with IPTG, no blue color was seen, even after extended growth in media containing X-GAL.

15 As an additional negative control, clones consisting of XL1-Blue MR transformed with the FLAG vector alone never showed any β -galactosidase activity with or without IPTG-induction, even after 7-days growth (Fig 10).

As a positive control for maximal β -galactosidase (derived from *E. coli* β -galactosidase) activity the cloning vector pGEM was transformed into the host strain DH5 α and the results are also shown in Figure 10. Figure 10 shows the detection of β -galactosidase activity from pZBG2-1-4 expression in *E. coli*.

5 Cells were harvested and extracts were prepared every 12 hours and the A₆₁₅ measured. Cultures were grown with the addition of the chromogenic substrate X-GAL (open symbols) or X-GAL and the transcriptional inducer IPTG (closed symbols) in the medium. The vector used as a positive control for *E. coli* β -galactosidase activity was pGEM (■) and the vector used as a negative control and for expression was pFLAG-CTC either without (○,●) or containing the pZBG2-1-4 ORF (Δ,▲).

Effects on Plant Tissue Texture

To further demonstrate the function of TBG4 encoded β -galactosidase II the following experiments were carried out.

Fruit from tomato plants containing antisense constructs to suppress TBG4 mRNA were up to 40% firmer [compare means of parental line #1 with antisense line #2 in Figures 11A – 11E(1-4)] than fruit from the parental line. Among the transformants the line with the firmest fruit also had the lowest overall levels of TBG4 mRNA (Figure 12A,B). This correlation suggests that a reduction in TBG4 mRNA is associated with increased fruit firmness. Firmer fruit might result in (1) less shipping damage (a) less loss due to damage and (b) ability to harvest at later stage resulting in better flavor at market (2) longer

shelf life for both market and consumer. (3) better quality fruit for fresh slice market; fruit cut better at the pink/red stage when firmer.

Methods

5 To determine the function of TBG4 encoded β -galactosidase II, antisense constructs were made using the constitutively expressed 35S CaMV promoter to express TBG4 antisense RNA (Figure 13). Constructs were moved into tomato using Agrobacterium-mediated transformation. Four tomato cultivars have been transformed in order to evaluate the effect of TBG4 suppression on processing tomato (cv 'UC82b') fruit paste quality and three fresh pick
10 cultivars. Of the fresh pick cultivars one is a soft fruit large cherry tomato (cv 'Ailsa Craig'), the second is a soft fruit old breeding line (cv 'Rutgers') and the third is a recently developed somewhat firm cultivar 'New Rutgers'. Among the lines where TBG4 mRNA is suppressed we expect to observe an
15 increase in firmness and paste viscosity.

Texture

Although this project is nearly finished the complete biochemical and molecular analysis is not finished. The preliminary results on the analysis of
20 the 'New Rutgers' cultivar is presented in Figures 11A – E(1-4) and 12A,B. In this example a fresh pick cultivar called 'New Rutgers' was used. Plants of the purchased seed were grown and allowed to self and the resulting seed was used as the parental control (line 1). Seven independent transformed plants (lines 2-8) containing TBG4 antisense constructs were grown and allowed to
25 self. Transformation (T-DNA insertion) was confirmed by southern analysis

(data not shown). From each transformed line, five plants were grown along with 10 parental line plants. Fruit were tagged at the breaker stage (1st onset of color change) and were harvested at breaker plus 7 days. Data were taken using 15-20 fruit from each line. Each type of texture measurement was done twice for each fruit and fruit were subjected to 4 types of texture measurements using a Stable Micro System's TA-XT2i texture analyzer. The 4 measurements were; 1, 2-inch flat plate compression to 3 mm (Figure 1A), 2, 4 mm spherical indenter compression to 3 mm (Figure 1B), 3, 4 mm cylindrical indenter compression to 3 mm (Figure 1C) and 4, 4 mm cylindrical indenter puncture to 10 mm (Figure 1D). The summary of this data is shown in Figure 1E(1-4). In Figures 1A -E (1-4) line 1 was the parental line and lines 2-8 each represent an independent transformant containing one T-DNA copy of the TBG4 antisense construct. Statistical analysis (Duncans and Scheffé) of the data revealed that fruit from the transformed lines 3, 7 and 8 were not significantly different from the parental line but that transformed lines 2, 4, 5 and 6 were significantly firmer than the parental fruit. Most noteworthy is that fruit from transformed line 2 had fruit with a mean firmness that was 40% firmer than that of the parental line (Figures 1A-D).

Northern Blot Analysis

We are currently investigating any changes in the biochemical composition of fruit where TBG4 mRNA levels have been suppressed. These experiments are designed to show a link between increased fruit firmness and TBG4 mRNA suppression, TBG4 encoded enzyme activity suppression,

possible cell wall modification (e.g. increased galactosyl residue content) and a decrease in free galactose levels during fruit ripening.

These experiments are not complete, however some preliminary Northern blot experiments were done and the data is shown in Figure 12A,B.

5 There is no parental or azygous control fruit RNA shown in Figure 12A,B because these plants were the last to grow, and RNA extractions are just being done now. As a comparison of normal fruit TBG4 mRNA levels refer to Figure 5 above. The data from Figure 5 showed that TBG4 mRNA levels are low at the mature green stage, peak at the turning stage and are reduced at the

10 red stage. All the lines except for 2 and 3 expressed antisense TBG4 mRNA (Figure 12A,B). The antisense transcripts appear as two bands, smaller in length than the endogenous mRNA. The two bands probably resulted from 1, the expected transcriptional stop signal provided by the NOS-terminator and 2, a cryptic transcriptional stop signal in the antisense TBG4 cDNA. The most

15 notable result was in line 2 where no TBG4 mRNA was detected at the turning stage. Line 2 also had the firmest red fruit (see Figure 11A -D). The absence of detectable TBG4 mRNA probably was the result of cosuppression of both the endogenous and antisense mRNAs. When compared to earlier blots (e.g. Figure 4), all of the lines appeared to have an overall reduced level of TBG4

20 mRNA, but it is impossible to assign numbers to this statement without the parental and azygous control RNA on the same Northern blot.

The specification discloses that β -galactosidase II polypeptide is involved in the degradation of cell wall pectin during fruit ripening. In the present invention, the role of β -galactosidases in tomato during fruit ripening and

25 softening and the description of the cloning of a β -galactosidase cDNA clone

that codes for a $\beta(1\rightarrow4)$ galactan degrading enzyme, which is expressed in ripening tomato fruit tissues, has been shown.

The present work indicates that pZBG2-1-4 is a cDNA derived from the transcript of the TBG4 gene which codes for β -galactosidase II for the following reasons:

First, the deduced amino acid sequence of the highly conserved amino-terminal portion of the expected mature pZBG2-1-4 translation product matches almost exactly (28 of 30 amino acids) with the amino-terminal sequence of β -galactosidase II as purified by Carey *et al.* (1995) and designated TOMAA. Importantly, the two amino acids (KY) in the β -galactosidase II sequence (TOMAA), that do not match the pZBG2-1-4 deduced amino acid sequence of the present invention are believed to be incorrect since all plant β -galactosidase sequences in the database and four additional β -galactosidase-related cDNAs that were identified from tomato all match or have conserved substitutions with the deduced amino acid sequence of pZBG2-1-4 at these same two amino acid (ST) positions (Figure 3).

Second, the transcript detected by pZBG2-1-4 is present in normal ripening fruit at the same time that β -galactosidase II activity was detected (Figure 5; Carey *et al.*, 1995). Moreover, little or no transcript was detected in fruit at 45 and 50 dpa from the mutants *nor*, *rin* and *Nr* (Figure 7). This observation also coincides with the data presented by Carey *et al.* (1995) that β -galactosidase II activity remained at levels equal to mature green fruit and did not rise in fruit 45-65 dpa from *nor* or *rin* plants. Interestingly, Carrington and Pressey (1996) have reported that β -galactosidase II activity was only

detected in 'Rutgers' fruit after the turning stage of ripeness. The Northern data in the present invention indicates that maximum β -galactosidase II activity occurs only after the turning stage, assuming mRNA levels predict extractable enzyme activity (Figure 5).

5 Third, the apparent molecular weight of 77.9 kD and pI of 8.9 for the mature protein predicted from the pZBG2-1-4 sequence is similar to that determined for β -galactosidase II. Pressey (1983), estimated a molecular weight of 62 kD by gel-filtration column chromatography and a pI of 7.8 by isoelectric focusing, while Carey *et al.* (1995) estimated a molecular weight of
10 75 kD by SDS-PAGE and a pI of 9.8 by isoelectric focusing.

Fourth, enzyme produced from pZBG2-1-4 ORF using a heterologous yeast expression system has both β -galactosidase activity and exogalactinase activity.

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What we claim is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

5 (a) a nucleotide sequence encoding the β -galactosidase II polypeptide having the complete amino acid sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO: 15 and SEQ ID NO: 16 and designated TBG1, TBG2, TBG3, TBG4, TBG5, TBG6 and TBG7, respectively as shown in Figure 2 or as encoded by the cDNA clone selected from the group consisting of cDNA clones contained in Gen Bank Accession No. AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422;

15 (b) a nucleotide sequence encoding the mature β -galactosidase II polypeptide having the amino acid sequence at about positions 24-724 selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and designated TBG1, TBG2, TBG3, TBG4, TBG5, TBG6 and TBG7, respectively as shown in Figure 2 or as encoded by the cDNA clone selected from the group consisting of cDNA clones contained in Gen Bank Accession No. AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422; and

20 (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b), above.

25 2. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7 as shown in Figure 2.

3. The nucleic acid molecule of claim 1 wherein said polynucleotide has the nucleotide sequence in Figure 2 (SEQ ID NO:4) encoding the β -galactosidase II polypeptide having the amino acid sequence designated TBG4 in Figure 2.

4. The nucleic acid molecule of claim 1 wherein said polynucleotide has the nucleotide sequence in Figure 2 (SEQ ID NO:4) encoding the mature polypeptide having the amino acid sequence from about 24 to about 724 in the amino acid sequence designated TBG4 in Figure 2.

5. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF023847.

6. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF154420.

7. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF154421.

8. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF020390.

9. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF154423.

10. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF154424.

11. The nucleic acid molecule of claim 1 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in Gen Bank Accession No. AF154422.

12. An isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a), (b), or (c) of claim 1 wherein said polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues.

13. An isolated nucleic acid molecule comprising a polynucleotide which encodes the amino acid sequence of an epitope-bearing portion of a β -galactosidase II polypeptide having an amino acid sequence in (a), (b), or (c) of claim 1.

14. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.

15. A recombinant vector produced by the method of claim 14.

16. A method of making a recombinant host cell comprising introducing the recombinant vector of claim 15 into a host cell.

17. A recombinant host cell produced by the method of claim 16.

18. A recombinant method for producing β -galactosidase II polypeptide, comprising culturing the recombinant host cell of claim 17 under conditions such that said polypeptide is expressed and recovering said polypeptide.

19. An isolated β -galactosidase II polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

a) amino acid sequence at about positions 24-724 selected from the group consisting of sequences SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and designated TBG1, TBG2, TBG3, TBG4, TBG5, TBG6 and TBG7, respectively as shown in Figure 2; and

b) amino acid sequence as encoded by the cDNA clone selected from the group consisting of cDNA clones contained in Gen Bank Accession No. AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422.

20. An isolated polypeptide comprising an epitope-bearing portion of the β -galactosidase II protein.

21. An isolated antibody that binds specifically to a β -galactosidase II polypeptide of claim 20.

22. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a nucleotide sequence encoding the β -galactosidase II polypeptide having the complete amino acid sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO: 15 and SEQ ID NO: 16 and designated TBG1, TBG2, TBG3, TBG4, TBG5, TBG6 and TBG7, respectively as shown in Figure 3 or as encoded by the cDNA clone selected from the group consisting of cDNA clones contained in Gen Bank Accession No. AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422;

(b) a nucleotide sequence encoding the mature β -galactosidase II polypeptide having the amino acid sequence at about positions 24-724 selected from the group consisting of sequences SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and designated TBG1, TBG2, TBG3, TBG4, TBG5, TBG6 and TBG7, respectively as shown in Figure 3 or as encoded by the cDNA clone selected from the group consisting of cDNA clones contained in Gen Bank Accession No. AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422; and

(c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b), above.

23. The nucleic acid molecule of claim 22 wherein said polynucleotide has a complete nucleotide sequence in Figure 2 selected from the group consisting of SEQ ID NOs: 1-3 and 5-7.

24. The nucleic acid molecule of claim 22 wherein said polynucleotide has a nucleotide sequence in Figure 2 selected from the group consisting of SEQ ID NOs: 1-3 and 5-7 encoding the β -galactosidase polypeptide having the complete amino acid sequence designated TBG1-3 and 5-7, respectively.

25. The nucleic acid molecule of claim 22 wherein said polynucleotide has the nucleotide sequence in Figure 2 selected from the group consisting of SEQ ID NOs: 1-3 and 5-7 encoding the mature polypeptide having the amino acid sequence designated TBG1-3 and 5-7, respectively.

26. The nucleic acid molecule of claim 22 wherein said polynucleotide has the complete nucleotide sequence of the cDNA clone contained in an Gen Bank Accession No. selected from the group consisting of ATCC Deposit No. selected from the group consisting of AF023847, AF154420, AF154421, AF020390, AF154423, AF154424 and AF154422.

27. A method of modifying cell wall metabolism in a plant which comprises transforming said plant with a DNA construct adapted to modify the activity of a β -galactosidase, growing said plant or its descendent and selecting a plant having modified cell wall characteristics, said construct comprising a transcriptional initiation region operative in plants operably linked to a DNA sequence encoding at least one β -galactosidase.

28. A method as claimed in claim 27, wherein said DNA sequence is selected from the group consisting of the sequences of nucleic acid molecules claimed in claim 1 or claim 22.

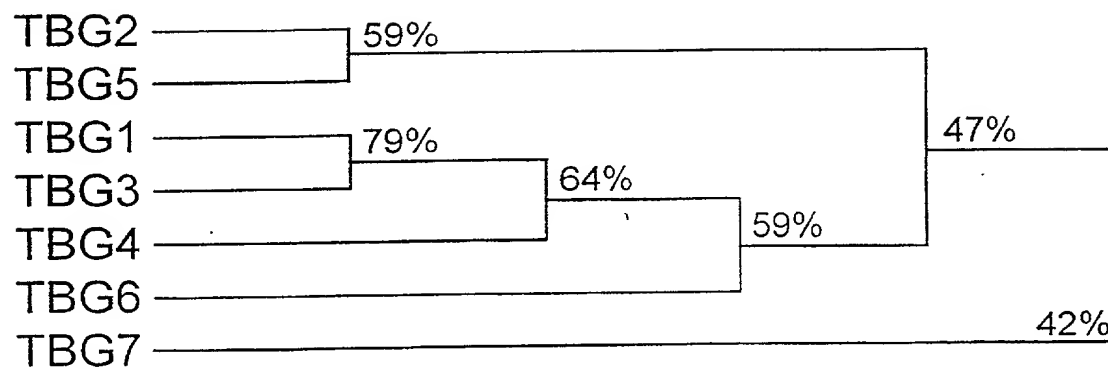
29. A plant cell transformed with a nucleic acid molecule as claimed in claim 1 or claim 22.

30. A plant derived from a plant cell as claimed in claim 29.

31. A plant seed derived from a plant as claimed in claim 30.

32. A method for modifying β -galactosidase gene expression in a plant comprising transforming said plant with a nucleic acid molecule as
5 claimed in claim 1 or claim 22, growing the transformed plant and selecting a plant having modified β -galactosidase gene expression when compared with an untransformed plant.

A



B

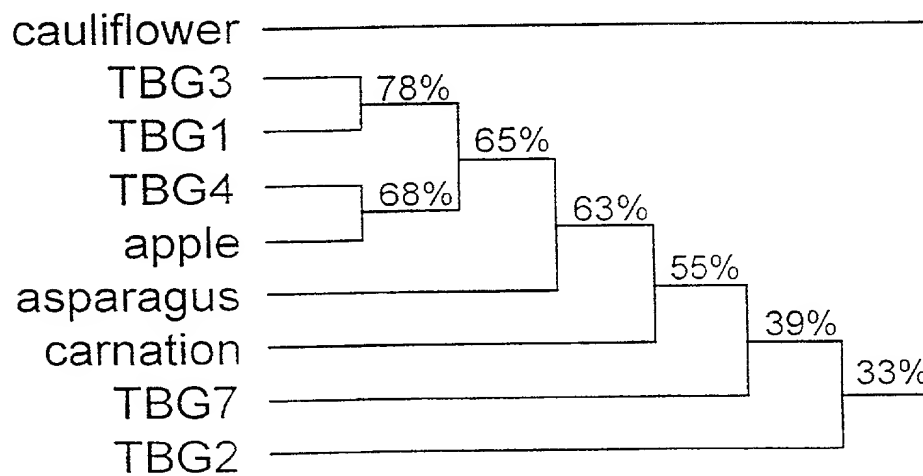


Figure 1. β -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato β -galactosidase (TBG) cDNAs. B. Plant β -galactosidases. Higgins-Sharp algorithm (UPGMA method)

Figure 2

Sheet 1 of 12

Gene/clone name: TBG1/pZBG2-1-10; accession number AF023847; Sequence ID number 1

TTTTCCTTTGTTCTTTTGCTCAGCACTAG 30
31 ACCCTAGAAGAGGAAAAAGAGTATGGACTAATGGAATAAACAATAAAAAAGAGAGAAAAAGAGAAAAAGAGAAATTCCTTCAGACAACA 122
123 AAAACAGCTGTTTTCCTTCACTACTTTTTCCTCCCAATCTCTATATAATGCAAGATAGAATAAAGTTTGCACTTGATTAATAAAAAA 214
215 GAATAATAAGCTGTGGGGTAGGGAGGAAGTTAGTTTCATTAGTTTCATTCGCTTGTAAAGGCACAATCTTGATTCTTGATTGTTGACAAAT 305

306 ATG GGT TTT TGG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TTA TGG GTT TCT TGT GGA ATT GCT TCT 374
1 Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser 23

375 GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC 443
24 Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His 46

444 TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT 512
47 Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Gly Val Asp Val 69

513 ATA CAG ACT TAT GTT TTC TGG AAT GGG CAT GAG CCT GAA GAA GGG AAA TAT TAT TTT GAA GAG AGG TAT 581
70 Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Gly Lys Tyr Tyr Phe Glu Glu Arg Tyr 92

582 GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT 650
93 Asp Leu Val Lys Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile Gly Pro Tyr 115

651 GCA TGT GCT GAA TGG AAT TTT GGG GGT TTT CCT GTT TGG CTG AAG TAT GTT CCA GGT ATT AGT TTC AGA 719
116 Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg 138

720 ACA AAC AAT GAG CCA TTC AAG GCT GCA ATG CAA AAG TTC ACT ACT AAG ATT GTT GAT ATG ATG AAA GCA 788
139 Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala 161

789 GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG 857
162 Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met 184

858 GAG TGG GAA CTA GGT GAA CCT GGT AAA GTT TAC TCA GAA TGG GCA GCC AAA ATG GCT GTG GAT CTT GGC 926
185 Glu Trp Glu Leu Gly Glu Pro Gly Lys Val Tyr Ser Glu Trp Ala Ala Lys Met Ala Val Asp Leu Gly 207

927 ACT GGT GTC CCA TGG ATC ATG TGC AAG CAA GAT GAT GTC CCT GAT CCT ATT ATT AAT ACT TGC AAT GGT 995
208 Thr Gly Val Pro Trp Ile Met Cys Lys Gln Asp Asp Val Pro Asp Pro Ile Ile Asn Thr Cys Asn Gly 230

996 TTC TAC TGT GAC TAC TTC ACA CCA AAT AAG GCT AAT AAA CCC AAG ATG TGG ACT GAA GCC TGG ACA GCC 1064
231 Phe Tyr Cys Asp Tyr Phe Thr Pro Asn Lys Ala Asn Lys Pro Lys Met Trp Thr Glu Ala Trp Thr Ala 253

1065 TGG TTT ACC GAA TTT GGA GGT CCA GTT CCT TAC CGT CCT GCA GAG GAT ATG GCA TTT GCT GTC GCA AGA 1133
254 Trp Phe Thr Glu Phe Gly Gly Pro Val Pro Tyr Arg Pro Ala Glu Asp Met Ala Phe Ala Val Ala Arg 276

1134 TTT ATA CAA ACG GGA GGC TCC TTC ATC AAT TAC TAT ATG TAT CAT GGA GGA ACA AAC TTT GGA AGG ACT 1202
277 Phe Ile Gln Thr Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr 299

1203 TCT GGT GGC CCA TTT ATT GCT ACT AGT TAT GAT TAT GAT GCA CCC CTA GAT GAA TTT GGG TCA TTA CGG 1271
300 Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Phe Gly Ser Leu Arg 322

1272 CAG CCT AAA TGG GGT CAT CTG AAA GAT CTA CAT AGA GCA ATA AAG CTC TGT GAG CCA GCT TTA GTA TCT 1340
323 Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala Leu Val Ser 345

1341 GTA GAT CCA ACT GTG ACA TCC TTA GGA AAC TAT CAA GAG GCA CGT GTT TTC AAG TCA GAG TCT GGG GCC 1409
346 Val Asp Pro Thr Val Thr Ser Leu Gly Asn Tyr Gln Glu Ala Arg Val Phe Lys Ser Glu Ser Gly Ala 368

1410 TGC GCT GCC TTC CTA GCA AAT TAC AAC CAG CAC TCT TTT GCT AAA GTG GCA TTT GGG AAC ATG CAT TAT 1478
369 Cys Ala Ala Phe Leu Ala Asn Tyr Asn Gln His Ser Phe Ala Lys Val Ala Phe Gly Asn Met His Tyr 391

1479 AAC TTG CCA CCC TGG TCT ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTC TAT AAT ACT GCA AGG GTT 1547
392 Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Tyr Asn Thr Ala Arg Val 414

1548 GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGT AGA GGA TTC TCA TGG GAG TCA TTC AAT GAA 1616
415 Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Phe Ser Trp Glu Ser Phe Asn Glu 437

Figure 2
Sheet 2 of 12

Gene/clone name: TBG1/pZBG210; accession number AF023847; Sequence ID number 1 cont.

1617 GAC GCA GCA TCG CRT GAA GAC GAC ACT TTC ACA GTT GTT GGG TTA TTG GAG CAG ATT AAT ATC ACA AGA	1685
438 Asp Ala Ala Ser His Glu Asp Asp Thr Phe Thr Val Val Gly Leu Leu Glu Gln Ile Asn Ile Thr Arg	460
1686 GAT GTA TCT GAT TAC TTG TGG TAT ATG ACT GAC ATT GAG ATT GAT CCA ACA GAA GGA TTT TTG AAT AGT	1754
461 Asp Val Ser Asp Tyr Leu Trp Tyr Met Thr Asp Ile Glu Ile Asp Pro Thr Glu Gly Phe Leu Asn Ser	483
1755 GGA AAT TGG CCT TGG CTT ACT GTC TTT TCT GCT GGC CAT GCA TTG CAT GTA TTC GTG AAT GGT CAA TTA	1823
484 Gly Asn Trp Pro Trp Leu Thr Val Phe Ser Ala Gly His Ala Leu His Val Phe Val Asn Gly Gln Leu	506
1824 GCA GGA ACT GTG TAC GGA AGT TTA GAA AAC CCA AAA CTA ACT TTC AGC AAC GGT ATA AAT CTG AGA GCT	1892
507 Ala Gly Thr Val Tyr Gly Ser Leu Glu Asn Pro Lys Leu Thr Phe Ser Asn Gly Ile Asn Leu Arg Ala	529
1893 GGT GTG AAC AAG ATT TCT CTG CTA AGC ATT GCT GTT GGT CTT CGG AAC GTT GGC CCT CAT TTT GAG ACA	1961
530 Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val Gly Leu Pro Asn Val Gly Pro His Phe Glu Thr	552
1962 TGG AAT GCT GGT GTT CTT GGA CCA GTT TCA CTT AAT GGA CTT AAT GAA GGA ACA AGA GAT TTA ACA TGG	2030
553 Trp Asn Ala Gly Val Leu Gly Pro Val Ser Leu Asn Gly Leu Asn Glu Gly Thr Arg Asp Leu Thr Trp	575
2031 CAG AAA TGG TTC TAC AAG GTT GGT CTA AAA GGA GAA GCC CTG AGT CTT CAT TCA CTC AGT GGT AGC CCA	2099
576 Gln Lys Trp Phe Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu Ser Leu His Ser Leu Ser Gly Ser Pro	598
2100 TCC GTG GAG TGG GTG GAA GGC TCT TTA GTG GCT CAG AAG CAG CCA CTC AGT TGG TAT AAG ACT ACA TTC	2168
599 Ser Val Glu Trp Val Glu Gly Ser Leu Val Ala Gln Lys Gln Pro Leu Ser Trp Tyr Lys Thr Thr Phe	621
2169 AAT GCT CCA GAT GGA AAT GAA CCT TTG GCT TTA GAT ATG AAT ACC ATG GGC AAA GGT CAA GTA TGG ATA	2237
622 Asn Ala Pro Asp Gly Asn Glu Pro Leu Ala Leu Asp Met Asn Thr Met Gly Lys Gly Gln Val Trp Ile	644
2238 AAT GGT CAG AGC CTC GGA CGC CAC TGG CCT GCA TAT AAA TCA TCT GGA AGT TGT AGT GTC TGT AAC TAT	2306
645 Asn Gly Gln Ser Leu Gly Arg His Trp Pro Ala Tyr Lys Ser Ser Gly Ser Cys Ser Val Cys Asn Tyr	667
2307 ACT GGC TGG TTT GAT GAG AAA AAG TGC CTA ACT AAC TGT GGT GAG GGC TCA CAA AGA TGG TAC CAC GTA	2375
668 Thr Gly Trp Phe Asp Glu Lys Lys Cys Leu Thr Asn Cys Gly Glu Gly Ser Gln Arg Trp Tyr His Val	690
2376 CCC CGG TCT TGG CTG TAT CCT ACT GGA AAT TTG TTA GTT GTA TTC GAG GAA TGG GGA GGA GAT CCT TAT	2444
691 Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asp Pro Tyr	713
2445 GGA ATC ACT TTA GTC AAA AGA GAA ATA GGG AGT GTT TGT GCT GAT ATA TAT GAG TGG CAA CCA CAG TTA	2513
714 Gly Ile Thr Leu Val Lys Arg Glu Ile Gly Ser Val Cys Ala Asp Ile Tyr Glu Trp Gln Pro Gln Leu	736
2514 TTG AAT TGG CAG AGG CTA GTA TCT GGT AAG TTT GAC AGA CCT CTC AGA CCT AAA GCC CAT CTT AAG TGT	2582
737 Leu Asn Trp Gln Arg Leu Val Ser Gly Lys Phe Asp Arg Pro Leu Arg Pro Lys Ala His Leu Lys Cys	759
2583 GCA CCT GGT CAG AAG ATT TCT TCA ATC AAA TTT GCA AGC TTT GGA ACA CCA GAG GGA GTT TGT GGG AAC	2651
760 Ala Pro Gly Gln Lys Ile Ser Ser Ile Lys Phe Ala Ser Phe Gly Thr Pro Glu Gly Val Cys Gly Asn	782
2652 TTC CAG CAG GGA AGC TGC CAT GCT CCG CGC TCA TAT GAT GCT TTC AAA AAG AAT TGT GTT GGG AAA GAG	2720
783 Phe Gln Gln Gly Ser Cys His Ala Pro Arg Ser Tyr Asp Ala Phe Lys Lys Asn Cys Val Gly Lys Glu	805
2721 TCT TGC TCA GTA CAG GTA ACA CCA GAG AAT TTT GGA GGT GAT CCA TGT CGA AAC GTT CTA AAG AAA CTC	2789
806 Ser Cys Ser Val Gln Val Thr Pro Glu Asn Phe Gly Gly Asp Pro Cys Arg Asn Val Leu Lys Lys Leu	828
2790 TCA GTG GAA GCC ATT TGT AGT TGA TGATTCAGAGTATACAAAGTGAAAAAATCTTGAACCACTCATATAACATTTTCAAACG	2873
829 Ser Val Glu Ala Ile Cys Ser ***	836
2874 AGCTACTAGACATCCATTAAACCCACACTACCATTTTTTGGCTTTGCTGGGGTTGAAGTTGTACAGTTAAGCAACACACCTCTTTGATCAAAG	2965
2966 CTCACCTGATTATGAAGATGATGACGAAAGATTCTGTACATGTAAGGTTTCGCTCTAATTACACATACAGATATGATTCTTGATGAATCGAT	3057
3058 GTGCAAAATTTGTTTGTGTTAGGGTGAGAGAGACTTGAAAAGCATTTTGCTTTTCATGATGTTCTACATTATACAATCATATGTAAGTAAGC	3149
3150 AAGCAATAATTCATTGCTTTGCACATTGAAAAATGCATTTTACTATGTTGCAGTACAAAAAATAAAAAAAAAAAAAA	3224

Figure 2

Sheet 3 of 12

Gene/clone name: TBG2/pZBG2-1-12; accession number AF154420; Sequence ID number 2

1	GG	2
3 AGC AGA AGA AAA ACA CTG AAT TTT CCG TTA ATA CTA ACG GTG TTA ACT ATC CAC TTT GTG ATC GTC GCC		71
1 Ser Arg Arg Lys Thr Leu Asn Phe Pro Leu Ile Leu Thr Val Leu Thr Ile His Phe Val Ile Val Ala		23
72 GGC GAG TAT TTC AAG CCG TTC AAT GTC ACC TAC GAT AAC CGA GCT CTC ATC ATC GGC GGT AAA CGC CGT		140
24 Gly Glu Tyr Phe Lys Pro Phe Asn Val Thr Tyr Asp Asn Arg Ala Leu Ile Ile Gly Gly Lys Arg Arg		46
141 ATG CTT ATC TCC GCC GGA ATT CAC TAC CCT CGC GCC ACT CCT GAG ATG TGG CCC ACA TTG ATA GCT AGG		209
47 Met Leu Ile Ser Ala Gly Ile His Tyr Pro Arg Ala Thr Pro Glu Met Trp Pro Thr Leu Ile Ala Arg		69
210 AGC AAA GAA GGT GGT GCA GAT GTC ATC GAG ACT TAT ACA TTT TGG AAT GGT CAT GAG CCA ACC AGG GGA		278
70 Ser Lys Glu Gly Gly Ala Asp Val Ile Glu Thr Tyr Thr Phe Trp Asn Gly His Glu Pro Thr Arg Gly		92
279 CAG TAC AAT TTT GAA GGA AGA TAT GAT ATT GTC AAG TTC GCA AAG CTA GTC GGA TCT CAT GGA CTG TTC		347
93 Gln Tyr Asn Phe Glu Gly Arg Tyr Asp Ile Val Lys Phe Ala Lys Leu Val Gly Ser His Gly Leu Phe		115
348 CTC TTT ATT CGA ATA GGT CCT TAT GCC TGT GCA GAA TGG AAC TTC GGG GGA TTC CCC ATA TGG CTT CGT		416
116 Leu Phe Ile Arg Ile Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Ile Trp Leu Arg		138
417 GAT ATA CCT GGA ATA GAA TTT CGA ACA GAT AAT GCA CCA TTC AAG GAG GAG ATG GAG CGC TAT GTT AAA		485
139 Asp Ile Pro Gly Ile Glu Phe Arg Thr Asp Asn Ala Pro Phe Lys Glu Glu Met Glu Arg Tyr Val Lys		161
486 AAG ATA GTT GAT CTT ATG ATA TCT GAG TCG CTC TTT TCG TGG CAA GGT GGT CCT ATC ATT TTG CTG CAG		554
162 Lys Ile Val Asp Leu Met Ile Ser Glu Ser Leu Phe Ser Trp Gln Gly Gly Pro Ile Ile Leu Leu Gln		184
555 ATT GAA AAT GAA TAT GGA AAT GTT GAA AGC TCA TTC GGT CCC AAG GGG AAG TTA TAT ATG AAA TGG GCT		623
185 Ile Glu Asn Glu Tyr Gly Asn Val Glu Ser Ser Phe Gly Pro Lys Gly Lys Leu Tyr Met Lys Trp Ala		207
624 GCT GAA ATG GCT GTT GGT CTT GGT GCT GGT GTT CCA TGG GTC ATG TGC AGG CAA ACT GAT GCT CCA GAA		692
208 Ala Glu Met Ala Val Gly Leu Gly Ala Gly Val Pro Trp Val Met Cys Arg Gln Thr Asp Ala Pro Glu		230
693 TAC ATC ATA GAT ACT TGT AAT GCA TAC TAT TGT GAT GGG TTC ACG CCG AAT TCC GAG AAG AAA CCG AAA		761
231 Tyr Ile Ile Asp Thr Cys Asn Ala Tyr Tyr Cys Asp Gly Phe Thr Pro Asn Ser Glu Lys Lys Pro Lys		253
762 ATT TGG ACT GAG AAT TGG AAT GGA TGG TTT GCA GAT TGG GGT GAA AGA CTT CCA TAT AGA CCT TCC GAG		830
254 Ile Trp Thr Glu Asn Trp Asn Gly Trp Phe Ala Asp Trp Gly Glu Arg Leu Pro Tyr Arg Pro Ser Glu		276
831 GAT ATT GCA TTT GCA ATT GCT CGT TTC TTT CAA CGT GGG GGC AGC TTA CAG AAC TAT TAT ATG TAT TTT		899
277 Asp Ile Ala Phe Ala Ile Ala Arg Phe Phe Gln Arg Gly Gly Ser Leu Gln Asn Tyr Tyr Met Tyr Phe		299
900 GGT GGG ACA AAT TTT GGC CGG ACT GCT GGT GGC CCA ACT CAA ATC ACT AGC TAT GAT TAT GAT GCT CCA		968
300 Gly Gly Thr Asn Phe Gly Arg Thr Ala Gly Gly Pro Thr Gln Ile Thr Ser Tyr Asp Tyr Asp Ala Pro		322
969 CTG GAT GAA TAT GGA CTA CTA CGT CAA CCT AAA TGG GGC CAT TTG AAG GAT CTG CAT GCT GCT ATA AAG		1037
323 Leu Asp Glu Tyr Gly Leu Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Ala Ala Ile Lys		345
1038 CTT TGT GAA CCA GCT CTT GTT GCT GCT GAT TCA CCT CAG TAT ATT AAA CTG GGA CCA AAA CAG GAG GCA		1106
346 Leu Cys Glu Pro Ala Leu Val Ala Ala Asp Ser Pro Gln Tyr Ile Lys Leu Gly Pro Lys Gln Glu Ala		368
1107 CAT GTC TAT CGT GGA ACA TCC AAC AAC ATT GGC CAA TAT ATG TCC TTA AAT GAA GGC ATA TGC GCA GCA		1175
369 His Val Tyr Arg Gly Thr Ser Asn Asn Ile Gly Gln Tyr Met Ser Leu Asn Glu Gly Ile Cys Ala Ala		391
1176 TTT ATT GCA AAT ATT GAT GAA CAT GAA TCA GCA ACA GTG AAA TTT TAC GGT CAA GAG TTC ACT TTA CCT		1244
392 Phe Ile Ala Asn Ile Asp Glu His Glu Ser Ala Thr Val Lys Phe Tyr Gly Gln Glu Phe Thr Leu Pro		414
1245 CCA TGG TCA GTG GTA TTC TGC CAG ATT GCA GAA ATA CAG CTT TCA ACA CAG CTA AGG TGG GGG CAC AAA		1313
415 Pro Trp Ser Val Val Phe Cys Gln Ile Ala Glu Ile Gln Leu Ser Thr Gln Leu Arg Trp Gly His Lys		437
1314 CTT CAA TCA AAA CAG TGG GCT CAG ATT CTG TTT CAG TTG GGA ATA ATT CTT TGT TTC TAC AAG TTA TCA		1382
438 Leu Gln Ser Lys Gln Trp Ala Gln Ile Leu Phe Gln Leu Gly Ile Ile Leu Cys Phe Tyr Lys Leu Ser		460

Figure 2
Sheet 4 of 12

Gene/clone name: TBG2/pZBG2-2; accession number AF154420; Sequence ID number 2 cont.

1383 CTA AAA GCA AGC TCG GAA AGT TTT TCA CAA TCT TGG ATG ACA TTG AAG GAG CCA CTT GGT GTG TGG GGT	1451
461 Leu Lys Ala Ser Ser Glu Ser Phe Ser Gln Ser Trp Met Thr Leu Lys Glu Pro Leu Gly Val Trp Gly	483
1452 GAC AAG AAT TTC ACT TCT AAA GGA ATA CTG GAG CAT CTG AAT GTG ACA AAA GAC CAG TCT GAT TAC CTG	1520
484 Asp Lys Asn Phe Thr Ser Lys Gly Ile Leu Glu His Leu Asn Val Thr Lys Asp Gln Ser Asp Tyr Leu	506
1521 TGG TAT CTG ACC AGG ATA TAT ATT TCT GAT GAT GAC ATC TCA TTT TGG GAG GAA AAT GAT GTT AGT CCA	1589
507 Trp Tyr Leu Thr Arg Ile Tyr Ile Ser Asp Asp Asp Ile Ser Phe Trp Glu Glu Asn Asp Val Ser Pro	529
1590 ACA ATT GAT ATT GAT AGC ATG CGT GAT TTT GTT CGC ATT TTT GTT AAT GGG CAG CTT GCA GGT AGT GTG	1658
530 Thr Ile Asp Ile Asp Ser Met Arg Asp Phe Val Arg Ile Phe Val Asn Gly Gln Leu Ala Gly Ser Val	552
1659 AAA GGC AAA TGG ATC AAG GTG GTT CAA CCT GTT AAG CTG GTT CAG GGA TAC AAC GAC ATA CTG CTA TTA	1727
553 Lys Gly Lys Trp Ile Lys Val Val Gln Pro Val Lys Leu Val Gln Gly Tyr Asn Asp Ile Leu Leu Leu	575
1728 TCT GAG ACG GTG GGA TTG CAG AAT TAT GGT GCC TTC TTG GAG AAG GAT GGG GCA GGT TTT AAA GGT CAG	1796
576 Ser Glu Thr Val Gly Leu Gln Asn Tyr Gly Ala Phe Leu Glu Lys Asp Gly Ala Gly Phe Lys Gly Gln	598
1797 ATA AAG CTT ACA GGA TGC AAA AGC GGG GAT ATC AAT CTC ACA ACA TCT TTA TGG ACC TAC CAG GTG GGG	1865
599 Ile Lys Leu Thr Gly Cys Lys Ser Gly Asp Ile Asn Leu Thr Thr Ser Leu Trp Thr Tyr Gln Val Gly	621
1866 CTT AGA GGC GAA TTC CTG GAA GTA TAT GAT GTC AAT AGT ACT GAA AGT GCA GGA TGG ACT GAG TTT CCC	1934
622 Leu Arg Gly Glu Phe Leu Glu Val Tyr Asp Val Asn Ser Thr Glu Ser Ala Gly Trp Thr Glu Phe Pro	644
1935 ACT GGT ACA ACT CCG TCA GTC TTT TCG TGG TAC AAG ACA AAG TTT GAT GCC CCA GGC GGG ACA GAT CCA	2003
645 Thr Gly Thr Thr Pro Ser Val Phe Ser Trp Tyr Lys Thr Lys Phe Asp Ala Pro Gly Gly Thr Asp Pro	667
2004 GTT GCT CTT GAT TTT AGT AGC ATG GGA AAA GGT CAG GCA TGG GTT AAT GGC CAC CAT GTA GGA AGA TAT	2072
668 Val Ala Leu Asp Phe Ser Ser Met Gly Lys Gly Gln Ala Trp Val Asn Gly His His Val Gly Arg Tyr	690
2073 TGG ACT TTG GTT GCA CCA AAT AAT GGA TGT GGA AGA ACT TGT GAT TAT CGT GGT GCT TAC CAC TCT GAT	2141
691 Trp Thr Leu Val Ala Pro Asn Asn Gly Cys Gly Arg Thr Cys Asp Tyr Arg Gly Ala Tyr His Ser Asp	713
2142 AAA TGT AGG ACA AAC TGT GGA GAG ATT ACT CAG GCC TGG TAC CAT ATA CCT AGA TCA TGG CTA AAG ACA	2210
714 Lys Cys Arg Thr Asn Cys Gly Glu Ile Thr Gln Ala Trp Tyr His Ile Pro Arg Ser Trp Leu Lys Thr	736
2211 TTA AAT AAT GTA CTA GTT ATC TTT GAA GAA ACA GAT AAA ACT CCG TTT GAT ATT TCC ATT TCT ACG CGT	2279
737 Leu Asn Asn Val Leu Val Ile Phe Glu Glu Thr Asp Lys Thr Pro Phe Asp Ile Ser Ile Ser Thr Arg	759
2280 TCT ACT GAA ACC ATT TGT GCT CAA GTA TCG GAA AAG CAC TAT CCA CCT CTA CAT AAG TGG TCT CAT TCG	2348
760 Ser Thr Glu Thr Ile Cys Ala Gln Val Ser Glu Lys His Tyr Pro Pro Leu His Lys Trp Ser His Ser	782
2349 GAG TTT GAC AGA AAG TTG TCT CTG ATG GAT AAA ACA CCA GAA ATG CAC TTG CAG TGT GAC GAA GGA CAT	2417
783 Glu Phe Asp Arg Lys Leu Ser Leu Met Asp Lys Thr Pro Glu Met His Leu Gln Cys Asp Glu Gly His	805
2418 ACA ATC TCT TCT ATT GAA TTT GCA AGC TAT GGA AGT CCG AAT GGC AGC TGT CAA AAG TTC TCA CAA GGA	2486
806 Thr Ile Ser Ser Ile Glu Phe Ala Ser Tyr Gly Ser Pro Asn Gly Ser Cys Gln Lys Phe Ser Gln Gly	828
2487 AAA TGC CAT GCT GCA AAT TCC TTG TCT GTT GTA TCT CAG GCT TGT ATA GGA AGA ACT AGT TGC AGC ATT	2555
829 Lys Cys His Ala Ala Asn Ser Leu Ser Val Val Ser Gln Ala Cys Ile Gly Arg Thr Ser Cys Ser Ile	851
2556 GGC ATT TCC AAT GGT GTA TTT GGA GAT CCA TGT CGA CAC GTT GTG AAG AGT TTG GCT GTT CAA GCA AAA	2624
852 Gly Ile Ser Asn Gly Val Phe Gly Asp Pro Cys Arg His Val Val Lys Ser Leu Ala Val Gln Ala Lys	874
2625 TGC TCA CCA CCA CCA GAC CTC AGC ACT TCA GCT TCC TCG TGA GGAGACTCTGTAACACGTTAACCTTTTGAACGAA	2702
875 Cys Ser Pro Pro Pro Asp Leu Ser Thr Ser Ala Ser Ser ***	888
2703 ACGATCCCTTAAAGTCCACTCGTTCCCTGCCCGAGCCCTCTGCTACATTTCTCAGATCGCATCGTTACAATCAGCCGGAGAAAACGTAC	2794
2795 ATGGACGATTTTACTTTGTAATATTTGGTTACTGTATATAAAATGAAAGGAATAATGTTGCTTATGCATATGAGCTGCAAAATTATATGACAA	2886
2887 AGTAACAAATGAAATAGAAAACCTCTGCTGTCAAGAAATTTTAAACAACACCATTTATTTAAAGTTAGTTAACATGATTAAAAA	2978
2979 AAAAAA	2984

Figure 2

Sheet 5 of 12

Gene/clone name: TBG3/p2-0c/bl; accession number AF154421; sequence ID number 3

1	AGAGTTCATTATTTTTCATTTTGAA	30
31	AAGAGGAAAAAATAAAGTTAAAGGGGGGAAAAAGTTTTCATTTTGCCCTAAAAAGGCACAATCTTGATAGAAAAGGAGATAATTTTAC	121
122	ATG GGT TGT ACG CTT ATA CTA ATG TTG AAT GTG TTG TTG GTG TTG GGT TCA TGG GTT TTT TCT GGA	190
1	Met Gly Cys Thr Leu Ile Leu Met Leu Asn Val Leu Leu Val Leu Leu Gly Ser Trp Val Phe Ser Gly	23
191	ACA GCT TCT GTT TCA TAT GAC CAT AGG GCT ATT ATT GTA AAT GGA CAA AGA AGA ATA CTT ATT TCT GGT	259
24	Thr Ala Ser Val Ser Tyr Asp His Arg Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser Gly	46
260	TCT GTT CAT TAT CCA AGA AGC ACT CCT GAG ATG TGG CCA GGT ATT ATT CAA AAG GCT AAA GAA GGA GGT	328
47	Ser Val His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys Ala Lys Glu Gly Gly	69
329	GTG GAT GTG ATT CAG ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CAA CAA GGG AAA TAT TAT TTT GAA	397
70	Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Gln Gln Gly Lys Tyr Tyr Phe Glu	92
398	GGG AGA TAT GAT TTA GTG AAG TTT ATT AAG CTG GTG CAC CAA GCA GGA CTT TAT GTC CAT CTT AGA GTT	466
93	Gly Arg Tyr Asp Leu Val Lys Phe Ile Lys Leu Val His Gln Ala Gly Leu Tyr Val His Leu Arg Val	115
467	GGA CCT TAT GCT TGT GCT GAA TGG AAT TTT GGG GGC TTT CCT GTT TGG CTG AAA TAT GTT CCA GGT ATC	535
116	Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile	138
536	AGT TTC AGA ACA GAT AAT GGA CCT TTC AAG GCT GCA ATG CAA AAA TTT ACT GCC AAG ATT GTC AAT ATG	604
139	Ser Phe Arg Thr Asp Asn Gly Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn Met	161
605	ATG AAA GCG GAA CGT TTG TAT GAA ACT CAA GGG GGG CCA ATA ATT TTA TCT CAG ATT GAG AAT GAA TAT	673
162	Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr	184
674	GGA CCC ATG GAA TGG GAA CTG GGA GCA CCA GGT AAA TCT TAC GCA CAG TGG GCC GCC AAA ATG GCT GTG	742
185	Gly Pro Met Glu Trp Glu Leu Gly Ala Pro Gly Lys Ser Tyr Ala Gln Trp Ala Ala Lys Met Ala Val	207
743	GGT CTT GAC ACT GGT GTC CCA TGG GTT ATG TGC AAG CAA GAC GAT GCC CCT GAT CCT ATT ATA AAT GCT	811
208	Gly Leu Asp Thr Gly Val Pro Trp Val Met Cys Lys Gln Asp Asp Ala Pro Asp Pro Ile Ile Asn Ala	230
812	TGC AAT GGC TTC TAC TGT GAC TAC TTT TCT CCA AAC AAG GCT TAT AAA CCA AAG ATA TGG ACT GAA GCC	880
231	Cys Asn Gly Phe Tyr Cys Asp Tyr Phe Ser Pro Asn Lys Ala Tyr Lys Pro Lys Ile Trp Thr Glu Ala	253
881	TGG ACT GCA TGG TTT ACT GGT TTT GGA AAT CCA GTT CCT TAC CGT CCT GCT GAG GAC TTG GCA TTT TCT	949
254	Trp Thr Ala Trp Phe Thr Gly Phe Gly Asn Pro Val Pro Tyr Arg Pro Ala Glu Asp Leu Ala Phe Ser	276
950	GTT GCA AAA TTT ATA CAG AAG GGA GGT TCC TTC ATC AAT TAT TAC ATG TAT CAT GGA GGA ACA AAC TTT	1018
277	Val Ala Lys Phe Ile Gln Lys Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe	299
1019	GGA CGG ACT GCT GGT GGT CCA TTT ATT GCT ACT AGT TAT GAC TAT GAT GCA CCA CTT GAT GAA TAT GGA	1087
300	Gly Arg Thr Ala Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly	322
1088	TTA TTG CGA CAA CCA AAA TGG GGT CAC CTG AAA GAT CTG CAT AGA GCA ATA AAG CTT TGT GAA CCA GCT	1156
323	Leu Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala	345
1157	TTA GTC TCT GGA GAT CCA GCT GTG ACA GCA CTT GGA CAC CAG CAG GAG GCC CAT GTT TTT AGG TCG AAG	1225
346	Leu Val Ser Gly Asp Pro Ala Val Thr Ala Leu Gly His Gln Gln Glu Ala His Val Phe Arg Ser Lys	368
1226	GCT GGC TCT TGT GCT GCA TTC CTT GCT AAC TAC GAC CAA CAC TCT TTT GCT ACT GTG TCA TTT GCA AAC	1294
369	Ala Gly Ser Cys Ala Ala Phe Leu Ala Asn Tyr Asp Gln His Ser Phe Ala Thr Val Ser Phe Ala Asn	391
1295	AGG CAT TAC AAC TTG CCA CCA TGG TCA ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTA TTT AAT ACA	1363
392	Arg His Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Phe Asn Thr	414
1364	GCA CGG ATC GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGC AGA GGA TTG CCC TGG CAG TCA	1432
415	Ala Arg Ile Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Leu Pro Trp Gln Ser	437
1433	TTC AAT GAA GAG ACA TCA TCT TAT GAA GAC AGT AGT TTT ACA GTT GTT GGG CTA TTG GAA CAG ATA AAT	1501
438	Phe Asn Glu Glu Thr Ser Ser Tyr Glu Asp Ser Ser Phe Thr Val Val Gly Leu Leu Glu Gln Ile Asn	460



Figure 2
Sheet 6 of 12

Gene/clone name: TBG3/p2-1-3/b1; accession number AF154421; Sequence ID number 3 cont.

1502	ACA ACA AGA GAC GTG TCT GAT TAT TTG TGG TAT TCA ACA GAT GTC AAG ATT GAT TCA AGA GAA AAG TTT	1570
461	Thr Thr Arg Asp Val Ser Asp Tyr Leu Trp Tyr Ser Thr Asp Val Lys Ile Asp Ser Arg Glu Lys Phe	483
1571	TTG AGA GGC GGA AAA TGG CCT TGG CTT ACG ATC ATG TCA GCT GGG CAT GCA TTG CAT GTT TTT GTG AAT	1639
484	Leu Arg Gly Gly Lys Trp Pro Trp Leu Thr Ile Met Ser Ala Gly His Ala Leu His Val Phe Val Asn	506
1640	GGT CAA TTA GCA GGA ACT GCA TAT GGA AGT TTA GAA AAA CCG AAA CTA ACT TTC AGT AAA GCC GTA AAT	1708
507	Gly Gln Leu Ala Gly Thr Ala Tyr Gly Ser Leu Glu Lys Pro Lys Leu Thr Phe Ser Lys Ala Val Asn	529
1709	CTG AGA GCA GGT GTT AAC AAG ATT TCT CTA CTG AGC ATT GCT GTT GGC CTT CCG AAT ATC GGC CCA CAT	1777
530	Leu Arg Ala Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val Gly Leu Pro Asn Ile Gly Pro His	552
1778	TTT GAG ACA TGG AAT GCT GGT GTT CTT GGG CCA GTC TCA CTA ACT GGT CTT GAC GAG GGG AAA AGA GAT	1846
553	Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val Ser Leu Thr Gly Leu Asp Glu Gly Lys Arg Asp	575
1847	TTA ACA TGG CAG AAA TGG TCT TAC AAG GTT GGT CTA AAA GGA GAA GCC TTG AGC CTC CAT TCA CTC AGT	1915
576	Leu Thr Trp Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu Ser Leu His Ser Leu Ser	598
1916	GGT AGC TCG TCA GTT GAG TGG GTC GAG GGT TCT TTA GTG GCT CAG AGA CAG CCA CTC ACA TGG TAC AAG	1984
599	Gly Ser Ser Ser Val Glu Trp Val Glu Gly Ser Leu Val Ala Gln Arg Gln Pro Leu Thr Trp Tyr Lys	621
1985	AGC ACT TTT AAT GCT CCA GCT GGA AAT GAT CCT TTG GCT TTA GAC TTG AAT ACC ATG GGC AAA GGA CAA	2053
622	Ser Thr Phe Asn Ala Pro Ala Gly Asn Asp Pro Leu Ala Leu Asp Leu Asn Thr Met Gly Lys Gly Gln	644
2054	GTG TGG ATA AAT GGT CAA AGC CTC GGA CGC TAT TGG CCT GGA TAT AAA GCA TCT GGT AAC TGC GGT GCC	2122
645	Val Trp Ile Asn Gly Gln Ser Leu Gly Arg Tyr Trp Pro Gly Tyr Lys Ala Ser Gly Asn Cys Gly Ala	667
2123	TGT AAC TAT GCA GGC TGG TTT AAT GAG AAA AAA TGC CTA AGT AAC TGT GGA GAG GCT TCA CAA CGA TGG	2191
668	Cys Asn Tyr Ala Gly Trp Phe Asn Glu Lys Lys Cys Leu Ser Asn Cys Gly Glu Ala Ser Gln Arg Trp	690
2192	TAT CAT GTT CCC CGT TCT TGG CTG TAT CCT ACT GGA AAT TTG TTA GTT CTA TTT GAG GAA TGG GGA GGA	2260
691	Tyr His Val Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu Leu Val Leu Phe Glu Glu Trp Gly Gly	713
2261	GAG CCT CAT GGA ATC TCT TTG GTA AAA AGA GAA GTT GCA AGT GTT TGT GCA GAT ATA AAC GAA TGG CAA	2329
714	Glu Pro His Gly Ile Ser Leu Val Lys Arg Glu Val Ala Ser Val Cys Ala Asp Ile Asn Glu Trp Gln	736
2330	CCA CAG TTG GTG AAT TGG CAA ATG CAA GCA TCT GGT AAA GTT GAC AAA CCA CTG AGA CCT AAA GCT CAC	2398
737	Pro Gln Leu Val Asn Trp Gln Met Gln Ala Ser Gly Lys Val Asp Lys Pro Leu Arg Pro Lys Ala His	759
2399	CTC TCG TGT GCT TCT GGT CAG AAG ATT ACT TCA ATC AAA TTT GCA AGC TTT GGA ACA CCA CAA GGG GTC	2467
760	Leu Ser Cys Ala Ser Gly Gln Lys Ile Thr Ser Ile Lys Phe Ala Ser Phe Gly Thr Pro Gln Gly Val	782
2468	TGC GGA AGC TTC CGT GAA GGA AGC TGC CAC GCC TTC CAC TCA TAT GAT GCT TTT GAA AGG TAT TGC ATC	2536
783	Cys Gly Ser Phe Arg Glu Gly Ser Cys His Ala Phe His Ser Tyr Asp Ala Phe Glu Arg Tyr Cys Ile	805
2537	GGG CAA AAC TCG TGC TCA GTA CCT GTA ACA CCA GAG ATC TTT GGA GGT GAT CCA TGT CCA CAT GTT ATG	2605
806	Gly Gln Asn Ser Cys Ser Val Pro Val Thr Pro Glu Ile Phe Gly Gly Asp Pro Cys Pro His Val Met	828
2606	AAG AAA CTC TCA GTT GAG GTT ATT TGC AGT TGA TGACACTGAGGAGAAACAATAAAAGTGGTTTCAGTTAGTTGTCTGAA	2686
829	Lys Lys Leu Ser Val Glu Val Ile Cys Ser ***	840
2687	CATATCAAAAAGTTGGCTTTGATGGAGGTGAAGTTGTACAGATATGCAACACACCTTTCCATTTGAGGCACATATGAATTGCAATGGCCCAA	2778
2779	GATTCGTACATATATGTTGGTTACTGTCAAGTTGGTATTTGGTATTTGCAAAATGTAACACAGTAGTATAGTCATTTGGTTCAAGTGGCATCGAG	2870
2871	ATTGTGCTAGTGGGAGGTAGTAGGTACCGATCGATCTATCGTTGTTTGCAACAAGCTGGGCTAGATTCCACTATTATTATAACAAAGAAAGC	2962
2963	ACAATGAGACTGATTCTTGATTAGTCCATGTGTAGATATTGTTACTGTGGAATTTGCAAAATCTTTGTGATTTTCAGCAAAAAAAAAAAAAA	3054
3055	AAAAAAAAAAAAAA	3069

Figure 2
Sheet 7 of 12one/clone name: TBG4/pZBG2-~~1~~pTomβgal4; accession number AF02039~~9~~ Sequence ID number 4

1	AAAAAAAAAGTTTCATTTTTCATAAAATAAAAAAAAAATTCATTTTTCGAATGTGGAAAAA	63
64	ATG CTA AGG ACT AAT GTG TTG TTG TTA TTA GTT ATT TGT TTA TTG GAT TTT TTT TCT TCA GTG AAA GCT	132
1	Met Leu Arg Thr Asn Val Leu Leu Leu Leu Val Ile Cys Leu Leu Asp Phe Phe Ser Ser Val Lys Ala	23
133	AGT GTT TCT TAT GAT GAC AGA GCT ATA ATC ATA AAT GGG AAA AGA AAA ATT CTT ATT TCT GGT TCA ATT	201
24	Ser Val Ser Tyr Asp Asp Arg Ala Ile Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile	46
202	CAT TAT CCA AGA AGC ACT CCA CAG ATG TGG CCT GAT CTT ATA CAA AAG GCT AAA GAT GGA GGC TTA GAT	270
47	His Tyr Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Asp Gly Gly Leu Asp	69
271	GTT ATT GAA ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT TCT CCT GGA AAA TAT AAT TTT GAA GGA AGA	339
70	Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg	92
340	TAT GAT CTT GTT AGA TTC ATC AAA ATG GTA CAA AGA GCA GGA CTT TAT GTC AAT TTA CGT ATT GGC CCT	408
93	Tyr Asp Leu Val Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg Ile Gly Pro	115
409	TAC GTC TGT GCT GAA TGG AAC TTT GGG GGA TTC CCT GTT TGG CTA AAA TAT GTG CCT GGT ATG GAA TTT	477
116	Tyr Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Met Glu Phe	138
478	AGA ACA AAC AAT CAG CCT TTT AAG GTG GCT ATG CAA GGA TTT GTT CAG AAA ATA GTC AAC ATG ATG AAG	546
139	Arg Thr Asn Asn Gln Pro Phe Lys Val Ala Met Gln Gly Phe Val Gln Lys Ile Val Asn Met Met Lys	161
547	TCA GAA AAT TTG TTT GAA TCT CAA GGA GGA CCA ATA ATT ATG GCC CAG ATA GAA AAT GAG TAT GGA CCA	615
162	Ser Glu Asn Leu Phe Glu Ser Gln Gly Gly Pro Ile Ile Met Ala Gln Ile Glu Asn Glu Tyr Gly Pro	184
616	GTA GAA TGG GAA ATT GGT GCT CCT GGT AAA GCT TAT ACA AAA TGG GCA GCT CAA ATG GCT GTA GGT TTG	684
185	Val Glu Trp Glu Ile Gly Ala Pro Gly Lys Ala Tyr Thr Lys Trp Ala Ala Gln Met Ala Val Gly Leu	207
685	AAA ACT GGT GTC CCA TGG ATC ATG TGT AAG CAA GAG GAT GCT CCT GAT CCT GTG ATT GAT ACT TGT AAT	753
208	Lys Thr Gly Val Pro Trp Ile Met Cys Lys Gln Glu Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn	230
754	GGC TTC TAC TGC GAA GGG TTC CGT CCT AAT AAG CCT TAC AAA CCT AAA ATG TGG ACA GAA GTA TGG ACT	822
231	Gly Phe Tyr Cys Glu Gly Phe Arg Pro Asn Lys Pro Tyr Lys Pro Lys Met Trp Thr Glu Val Trp Thr	253
823	GGC TGG TAT ACG AAA TTC GGT GGT CCA ATT CCT CAA AGA CCA GCC GAA GAC ATT GCA TTT TCA GTT GCC	891
254	Gly Trp Tyr Thr Lys Phe Gly Gly Pro Ile Pro Gln Arg Pro Ala Glu Asp Ile Ala Phe Ser Val Ala	276
892	AGG TTT GTT CAG AAC AAT GGT TCA TTC TTC AAT TAC TAC ATG TAT CAT GGA GGA ACA AAT TTT GGC CGG	960
277	Arg Phe Val Gln Asn Asn Gly Ser Phe Phe Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg	299
961	ACA TCA TCA GGG CTT TTC ATT GCA ACT AGC TAC GAT TAT GAT GCT CCT CTC GAT GAA TAT GGG TTG CTG	1029
300	Thr Ser Ser Gly Leu Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly Leu Leu	322
1030	AAT GAA CCA AAG TAT GGG CAC TTG AGA GAC TTA CAT AAA GCT ATC AAG CTA TCT GAA CCG GCT TTA GTT	1098
323	Asn Glu Pro Lys Tyr Gly His Leu Arg Asp Leu His Lys Ala Ile Lys Leu Ser Glu Pro Ala Leu Val	345
1099	TCA TCA TAT GCT GCG GTG ACT AGT CTT GGA AGT AAT CAA GAG GCT CAT GTT TAT AGA TCA AAA TCT GGA	1167
346	Ser Ser Tyr Ala Ala Val Thr Ser Leu Gly Ser Asn Gln Glu Ala His Val Tyr Arg Ser Lys Ser Gly	368
1168	GCT TGT GCT GCT TTT TTA TCC AAC TAT GAC TCT AGA TAT TCA GTA AAA GTC ACC TTT CAG AAT AGG CCA	1236
369	Ala Cys Ala Ala Phe Leu Ser Asn Tyr Asp Ser Arg Tyr Ser Val Lys Val Thr Phe Gln Asn Arg Pro	391
1237	TAC AAT CTG CCT CCA TGG TCC ATC AGC ATT CTT CCC GAC TGC AAA ACT GCC GTT TAC AAC ACT GCA CAG	1305
392	Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Thr Ala Val Tyr Asn Thr Ala Gln	414
1306	GTT AAC TCT CAA AGC TCG AGC ATA AAG ATG ACG CCT GCA GGT GGT GGA TTG TCT TGG CAG TCA TAC AAT	1374
415	Val Asn Ser Gln Ser Ser Ser Ile Lys Met Thr Pro Ala Gly Gly Gly Leu Ser Trp Gln Ser Tyr Asn	437
1375	GAA GAA ACG CCT ACT GCT GAT GAC AGC GAT ACA CTT ACA GCT AAC GGA CTA TGG GAA CAG AAA AAC GTC	1443
438	Glu Glu Thr Pro Thr Ala Asp Asp Ser Asp Thr Leu Thr Ala Asn Gly Leu Trp Glu Gln Lys Asn Val	460

Figure 2
Sheet 8 of 12Gene/clone name: TBG4/pZBG2-/pTomβgal4; accession number AF0203 Sequence ID number 4
cont.

1444	ACA AGA GAT TCA TCA GAC TAT CTG TGG TAC ATG ACA AAT GTA AAT ATA GCA TCT AAT GAA GGA TTT CTA	1512
461	Thr Arg Asp Ser Ser Asp Tyr Leu Trp Tyr Met Thr Asn Val Asn Ile Ala Ser Asn Glu Gly Phe Leu	483
1513	AAG AAC GGA AAG GAT CCT TAT CTC ACT GIT ATG TCC GCT GGT CAT GTC TTG CAT GTT TTC GTC AAT GGA	1581
484	Lys Asn Gly Lys Asp Pro Tyr Leu Thr Val Met Ser Ala Gly His Val Leu His Val Phe Val Asn Gly	506
1582	AAA CTA TCA GGA ACT GTT TAT GGT ACA TTG GAT AAT CCA AAA CTT ACA TAC AGT GGC AAC GTG AAG TTA	1650
507	Lys Leu Ser Gly Thr Val Tyr Gly Thr Leu Asp Asn Pro Lys Leu Thr Tyr Ser Gly Asn Val Lys Leu	529
1651	AGA GCT GGT ATT AAC AAG ATT TCT CTG CTC AGT GTT TCC GTT GGT CTC CCG AAC GTT GGC GTG CAT TAT	1719
530	Arg Ala Gly Ile Asn Lys Ile Ser Leu Leu Ser Val Ser Val Gly Leu Pro Asn Val Gly Val His Tyr	552
1720	GAT ACA TGG AAT GCA GGA GTT CTA GGT CCA GTC ACG TTG AGC GGT CTC AAT GAA GGG TCA AGA AAC TTG	1788
553	Asp Thr Trp Asn Ala Gly Val Leu Gly Pro Val Thr Leu Ser Gly Leu Asn Glu Gly Ser Arg Asn Leu	575
1789	GGG AAA CAG AAA TGG TCT TAC AAG GTT GGT CTG AAA GGC GAA TCG TTA AGT CTT CAC TCC TTA AGT GGG	1857
576	Ala Lys Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser Leu Ser Gly	598
1858	AGT TCT TCT GTT GAA TGG GTT CGA GGT TCA CTA ATG GCT CAA AAG CAG CCC CTG ACT TGG TAC AAG GCT	1926
599	Ser Ser Ser Val Glu Trp Val Arg Gly Ser Leu Met Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Ala	621
1927	ACA TTT AAC GCG CTT GGA GGA AAT GAT CCA CTA ATG GCT CAA AAG CAG CCC CTG ACT TGG TAC AAG GCT	1995
622	Thr Phe Asn Ala Pro Gly Gly Asn Asp Pro Leu Ala Leu Asp Met Ala Ser Met Gly Lys Gly Gln Ile	644
1996	TGG ATA AAT GGT GAA GGC GTA GGT CGC CAT TGG CCT GGA TAC ATA GCA CAA GGC GAC TGC AGC AAA TGC	2064
645	Trp Ile Asn Gly Glu Gly Val Gly Arg His Trp Pro Gly Tyr Ile Ala Gln Gly Asp Cys Ser Lys Cys	667
2065	AGT TAT GCT GGA ACG TTC AAC GAG AAG AAG TGC CAG ACT AAC TGC GGA CAA CCT TCT CAG AGA TGG TAC	2133
668	Ser Tyr Ala Gly Thr Phe Asn Glu Lys Lys Cys Gln Thr Asn Cys Gly Gln Pro Ser Gln Arg Trp Tyr	690
2134	CAT GTT CCA CGA TCG TGG CTG AAA CCA AGT GGA AAC TTG TTA GTA GTA TTC GAA GAA TGG GGA GGT AAT	2202
691	His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asn	713
2203	CCA ACA GGA ATT TCT CTA GTC AGG AGA TCA AGA TAA AGAACTCGAAAAGTAAAACCTTGTTTCAGTAACTATGGTGCTTGAA	2282
714	Pro Thr Gly Ile Ser Leu Val Arg Arg Ser Arg ***	725
2283	TTGCGCCGAAAAATACATACACGAAGCTAACATGGAGGCTACAGTTTGCAAATTCAGCTGAATAAAACATTAGAAGATAAAGAAATATT	2374
2375	TGATTAAAGGAGTATATAAATTTACAGAGAATTTTCTTTATTCCTTTGTAAACTTTGGTTTATAAAGTTTATACAGAATTTCTGTATT	2466
2467	GGATTATGAGATTGAAGAAGATTGTACAGCTTCCAAATACTATTAGAATACAATAAATTTTCATGTAAAAA	2554

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Figure 2
Sheet 9 of 12

Gene/clone name: TBG5/RT-PCR2-1/b1; accession number AF154423; sequence ID number 5

1	ATC CAG ACT TAC GTT TTC TGG AAC CTT CAT GAA CCT GTT CGA AAT CAG TAT GAT TTT GAA GGA AGG AAA	69
1	Ile Gln Thr Tyr Val Phe Trp Asn Leu His Glu Pro Val Arg Asn Gln Tyr Asp Phe Glu Gly Arg Lys	23
70	GAT TTG ATT AAT TTT GTG AAG TTG GTG GAG AGA GCT GGC TTA TTT GTT CAT ATA AGG ATT GGG CCT TAT	138
24	Asp Leu Ile Asn Phe Val Lys Leu Val Glu Arg Ala Gly Leu Phe Val His Ile Arg Ile Gly Pro Tyr	46
139	GTT TGT GCA GAA TGG AAC TAT GGT GGG TTT CCT CTT TGG TTG CAT TTC ATT CCT GGA ATT GAA TTT CGA	207
47	Val Cys Ala Glu Trp Asn Tyr Gly Gly Phe Pro Leu Trp Leu His Phe Ile Pro Gly Ile Glu Phe Arg	69
208	ACC GAC AAT GAA CCG TTC AAG GCA GAA ATG AAG CGA TTC ACA GCT AAA ATT GTT GAC ATG ATC AAG CAA	276
70	Thr Asp Asn Glu Pro Phe Lys Ala Glu Met Lys Arg Phe Thr Ala Lys Ile Val Asp Met Ile Lys Gln	92
277	GAA AAT CTA TAT GCA TCC CAG GGT GGG CCG GTT ATC TTG TCT CAG ATA GAA AAT GAG TAT GGC AAT GGT	345
93	Glu Asn Leu Tyr Ala Ser Gln Gly Gly Pro Val Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Asn Gly	115
346	GAT ATT GAG TCT CGT TAT GGT CCT CGT GCC AAA CCT TAC GTG AAC TGG GCA GCA TCA ATG GCT ACG TCT	414
116	Asp Ile Glu Ser Arg Tyr Gly Pro Arg Ala Lys Pro Tyr Val Asn Trp Ala Ala Ser Met Ala Thr Ser	138
415	TTA AAT ACG GGA GTG CCA TGG GTT ATG TGT CAG CAA CCA GAT GCC CCT CCT TCC GTT ATT AAC ACT TGC	483
139	Leu Asn Thr Gly Val Pro Trp Val Met Cys Gln Gln Pro Asp Ala Pro Pro Ser Val Ile Asn Thr Cys	161
484	AAT GGA TTT TAT TGT GAC CAA TTC AAG CAA AAT TCC GAT AAA ACA CCC AAG ATG TGG ACT GAG AAT TGG	552
162	Asn Gly Phe Tyr Cys Asp Gln Phe Lys Gln Asn Ser Asp Lys Thr Pro Lys Met Trp Thr Glu Asn Trp	184
553	ACC GGA TGG TTT CTG TCG TTT GGT GGT CCT GTC CCT TAC AGA CCA GTG GAA GAC ATC GCT TTC GCT GTG	621
185	Thr Gly Trp Phe Leu Ser Phe Gly Gly Pro Val Pro Tyr Arg Pro Val Glu Asp Ile Ala Phe Ala Val	207
622	GCT CGA TTT TTC CAG CGA GGC GGA ACT TTC CAG AAC TAT TAC ATG TAC CAC GGG GGA ACT AAC TTT GGG	690
208	Ala Arg Phe Phe Gln Arg Gly Gly Thr Phe Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly	230
691	AGA ACC AGT GGT GGA CCG TTT ATT GCA ACT AGC TAT GAC TAT GAT GCC CCT CTC GAC GAA TAC GG	755
231	Arg Thr Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr	252

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Figure 2

Sheet 10 of 12

Gene/clone name: TBG6/RT-R2-6/bl; accession number AF154424; Sequence ID number 8

1 ATC CAG ACA TAT GTT TTT TGG AAT GTT CAT GAG CCT TCT CCT GGC AAT TAC AAT TTT GAA GGA AGA TAT	69
1 Ile Gln Thr Tyr Val Phe Trp Asn Val His Glu Pro Ser Pro Gly Asn Tyr Asn Phe Glu Gly Arg Tyr	23
70 GAC CTG GTG AGG TTT GTA AAA ACG ATT CAG AAA GCA GGG CTG TAT GCT CAT CTT CGA ATT GGC OCT TAC	138
24 Asp Leu Val Arg Phe Val Lys Thr Ile Gln Lys Ala Gly Leu Tyr Ala His Leu Arg Ile Gly Pro Tyr	46
139 GTT TGT GCA GAG TGG AAT TTT GGA GGG TTT CCA GTA TGG CTG AAG TAT GTA CCT GGC ATT AGC TTC AGA	207
47 Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg	69
208 GCT GAT AAT GAA CCT TTC AAG AAC GCA ATG AAA GGG TAT GCT GAG AAA ATT GTT AAC TTG ATG AAG ATC	276
70 Ala Asp Asn Glu Pro Phe Lys Asn Ala Met Lys Gly Tyr Ala Glu Lys Ile Val Asn Leu Met Lys Ile	92
277 ATA ATC TTT TCG AGT CTC AGG GTG GTC CAA TCA TAC TCT CAC AGA TTG AGA ATG AGT ATG GGC CTC AAG	345
93 Ile Ile Phe Ser Ser Leu Arg Val Val Gln Ser Tyr Ser His Arg Leu Arg Met Ser Met Gly Leu Lys	115
346 CCA AGG TAC TTG GAG CAC CGG GAC ATC AGT ATT CAA CAT GGG CTG CAA ATA TGG CAG TTG GAT TTG AAC	414
116 Pro Arg Tyr Leu Glu His Arg Asp Ile Ser Ile Gln His Gly Leu Gln Ile Trp Gln Leu Asp Leu Asn	138
415 ACA GGC GTC CCA TGG GTG ATG TGC AAG GAA GAA GAT GCA CCA GAT CCT GTG ATC AAC ACA TGC AAT GGT	483
139 Thr Gly Val Pro Trp Val Met Cys Lys Glu Glu Asp Ala Pro Asp Pro Val Ile Asn Thr Cys Asn Gly	161
484 TTC TAC TGT GAT AAT TTC TTC CCA AAC AAA CCA TAC AAA CCT GCA ATT TGG ACT GAA GCT TGG AGT GGA	552
162 Phe Tyr Cys Asp Asn Phe Phe Pro Asn Lys Pro Tyr Lys Pro Ala Ile Trp Thr Glu Ala Trp Ser Gly	184
553 TGG TTC TCG GAA TTT GGC GGT CCC CTT CAT CAG AGA CCA GTT CAG GAT TTG GCA TTT GCT GTT GCC CAA	621
185 Trp Phe Ser Glu Phe Gly Gly Pro Leu His Gln Arg Pro Val Gln Asp Leu Ala Phe Ala Val Ala Gln	207
622 TTT ATA CAA AGA GGA GGA TCT TTT GTT AAC TAT TAC ATG TAC CAT GGG GGC ACG AAC TTT GGA GGC ACT	690
208 Phe Ile Gln Arg Gly Gly Ser Phe Val Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr	230
691 GCG GGT GGG CCA TTC ATC ACT ACC AGC TAT GAT TAT GAT GCC CCC CTC GAC GAG TAT GG	749
231 Ala Gly Gly Pro Phe Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr	250

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Figure 2
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Gene/clone name: TBG7/102-1-18; accession number AF154422; sequence number 7

1	GCACCTCTCCG	12
13	GTGAATAACACCGGTAAACGGCCCAATGCCAACTCTCGTCGGAATCTGAATAGTGATTTAAGCAGCTTAGCTAGCTAACTTTTGCTCTGCA	103
104	ATG AAC ACA ATG AGT TGT TTG TCC TCT AAT TTC AAG TTC GTT TTC CTT GCC TCG ACT GTG ATA TGG ATG	172
1	Met Asn Thr Met Ser Cys Leu Ser Ser Asn Phe Lys Phe Val Phe Leu Ala Ser Thr Val Ile Trp Met	23
173	ACG GTA ATG TCG TCG TCG TTA GCA GCA GTA GAT GCT TCC AAT GTT ACT ACT ATT GGT ACT GAT AGT GTG	241
24	Thr Val Met Ser Ser Ser Leu Ala Ala Val Asp Ala Ser Asn Val Thr Thr Ile Gly Thr Asp Ser Val	46
242	ACT TAC GAT CGA CGC TCG TTG ATT ATT AAC GGC CAG AGG AAG CTG CTC ATC TCC GCT TCC ATT CAC TAT	310
47	Thr Tyr Asp Arg Arg Ser Leu Ile Ile Asn Gly Gln Arg Lys Leu Leu Ile Ser Ala Ser Ile His Tyr	69
311	CCT CGC AGT GTC CCT GCC ATG TGG CCT GGT CTG GTT CGA TTG GCG AAG GAA GGA GGA GTG GAT GTT ATT	379
70	Pro Arg Ser Val Pro Ala Met Trp Pro Gly Leu Val Arg Leu Ala Lys Glu Gly Gly Val Asp Val Ile	92
380	GAA ACG TAT GTT TTC TGG AAC GGT CAC GAA CCT TCT CCG GGC AAT TAT TAC TTT GGA GGA AGG TTT GAT	448
93	Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Asn Tyr Tyr Phe Gly Gly Arg Phe Asp	115
449	CTA GTC AAA TTT TGT AAG ATC ATT CAG CAG GCT GGA ATG TAT ATG ATT CTT CGG ATT GGA CCA TTT GTA	517
116	Leu Val Lys Phe Cys Lys Ile Ile Gln Gln Ala Gly Met Tyr Met Ile Leu Arg Ile Gly Pro Phe Val	138
518	GCT GCA GAA TGG AAC TTT GGT GGA CTT CCT GTG TGG TTG CAT TAT GTG CCA GGT ACC ACC TTT CGG ACT	586
139	Ala Ala Glu Trp Asn Phe Gly Gly Leu Pro Val Trp Leu His Tyr Val Pro Gly Thr Thr Phe Arg Thr	161
587	GAT AGT GAA CCA TTT AAG TAT CAC ATG CAG AAG TTC ATG ACA TAT ACA GTG AAC TTA ATG AAG AGA GAG	655
162	Asp Ser Glu Pro Phe Lys Tyr His Met Gln Lys Phe Met Thr Tyr Thr Val Asn Leu Met Lys Arg Glu	184
656	AGG CTT TTT GCA TCT CAA GGA GGT CCA ATC ATC TTG TCA CAG GTA GAA AAT GAG TAC GGC TAC TAT GAA	724
185	Arg Leu Phe Ala Ser Gln Gly Gly Pro Ile Ile Leu Ser Gln Val Glu Asn Glu Tyr Gly Tyr Tyr Glu	207
725	AAT GCA TAT GGA GAA GGA GGG AAA AGG TAT GCC TTA TGG GCT GCT AAA ATG GCC CTT TCT CAA AAT ACT	793
208	Asn Ala Tyr Gly Glu Gly Gly Lys Arg Tyr Ala Leu Trp Ala Ala Lys Met Ala Leu Ser Gln Asn Thr	230
794	GGT GTA CCT TGG ATA ATG TGC CAG CAG TAT GAT GCT CCT GAT CCT GTG ATT GAC ACA TGC AAT TCA TTT	862
231	Gly Val Pro Trp Ile Met Cys Gln Gln Tyr Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn Ser Phe	253
863	TAC TGC GAC CAA TTT AAA CCA ATC TCT CCA AAC AAG CCC AAA ATT TGG ACA GAG AAC TGG CCG GGA TGG	931
254	Tyr Cys Asp Gln Phe Lys Pro Ile Ser Pro Asn Lys Pro Lys Ile Trp Thr Glu Asn Trp Pro Gly Trp	276
932	TTC AAG ACA TTT GGG GCC AGA GAT CCT CAC AGG CCT GCA GAA GAT GTT GCT TAT TCC GTG GCT CGT TTT	1000
277	Phe Lys Thr Phe Gly Ala Arg Asp Pro His Arg Pro Ala Glu Asp Val Ala Tyr Ser Val Ala Arg Phe	299
1001	TTC CAA AAA GGA GGA AGC GTG CAG AAT TAT TAC ATG TAC CAT GGT GGG ACG AAC TTT GGC AGG ACA GCA	1069
300	Phe Gln Lys Gly Gly Ser Val Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr Ala	322
1070	GGT GGC CCT TTC ATT ACC ACA AGT TAT GAC TAT GAT GCC CCA ATT GAC GAA TAT GGT TTA CCA AGG TTT	1138
323	Gly Gly Pro Phe Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Asp Glu Tyr Gly Leu Pro Arg Phe	345
1139	CCA AAA TGG GGT CAC CTT AAA GAA CTT CAT AAA GTC ATA AAA TCG TGT GAG CAT GCT CTG CTG AAC AAT	1207
346	Pro Lys Trp Gly His Leu Lys Glu Leu His Lys Val Ile Lys Ser Cys Glu His Ala Leu Leu Asn Asn	368
1208	GAT CCA ACT CTT CTT TCA TTA GGT CCT CTA CAA GAG GCT GAT GTT TAT GAA GAT GCT TCA GGC GCT TGT	1276
369	Asp Pro Thr Leu Leu Ser Leu Gly Pro Leu Gln Glu Ala Asp Val Tyr Glu Asp Ala Ser Gly Ala Cys	391
1277	GCT GCC TTT CTC GCG AAT ATG GAT GAC AAA AAT GAC AAG GTG GTA CAG TTC CGA CAT GTA TCA TAC CAC	1345
392	Ala Ala Phe Leu Ala Asn Met Asp Asp Lys Asn Asp Lys Val Val Gln Phe Arg His Val Ser Tyr His	414
1346	TTG CCA GCA TGG TCT GTT AGC ATT TTG CCA GAC TGC AAA AAT GTA GCG TTC AAC ACA GCA AAG GTT GGA	1414
415	Leu Pro Ala Trp Ser Val Ser Ile Leu Pro Asp Cys Lys Asn Val Ala Phe Asn Thr Ala Lys Val Gly	437
1415	TGT CAA ACT TCT ATT GTC AAT ATG GCA CCC ATA GAT TTG CAT CCC ACC GCA AGT TCA CCA AAG AGA GAC	1483
438	Cys Gln Thr Ser Ile Val Asn Met Ala Pro Ile Asp Leu His Pro Thr Ala Ser Ser Pro Lys Arg Asp	460

Figure 2
Sheet 12 of 12

Gene/clone name: TBG7/pZBG-18; accession number AF154422; Sequence ID number 7 cont.

1484 ATC AAG TCT CTT CAG TGG GAA GTC TTC AAG GAA ACA GCT GGA GTA TGG GGA GTT GCT GAT TTC ACT AAA	1552
461 Ile Lys Ser Leu Gln Trp Glu Val Phe Lys Glu Thr Ala Gly Val Trp Gly Val Ala Asp Phe Thr Lys	483
1553 AAC GGA TTT GTA GAT CAC ATT AAC ACC ACA AAA GAT GCT ACA GAC TAC CTC TGG TAC ACA ACA AGT ATT	1621
484 Asn Gly Phe Val Asp His Ile Asn Thr Thr Lys Asp Ala Thr Asp Tyr Leu Trp Tyr Thr Thr Ser Ile	506
1622 TTT GTT CAT GCA GAG GAG GAT TTC CTA AGA AAC AGA GGC ACT GCA ATG CTT TTC GTT GAA TCA AAG GGT	1690
507 Phe Val His Ala Glu Glu Asp Phe Leu Arg Asn Arg Gly Thr Ala Met Leu Phe Val Glu Ser Lys Gly	529
1691 CAT GCT ATG CAT GTC TTC ATC AAT AAA AAG CTT CAA GCC AGT GCA TCT GGA AAT GGC ACA GTG CCA CAG	1759
530 His Ala Met His Val Phe Ile Asn Lys Lys Leu Gln Ala Ser Ala Ser Gly Asn Gly Thr Val Pro Gln	552
1760 TTC AAG TTT GGA ACT CCT ATT GCT CTA AAG GCA GGG AAG AAT GAA ATT TCC TTG TTA AGC ATG ACT GTG	1828
553 Phe Lys Phe Gly Thr Pro Ile Ala Leu Lys Ala Gly Lys Asn Glu Ile Ser Leu Leu Ser Met Thr Val	575
1829 GGC CTA CAA ACA GCT GGA GCG TTT TAT GAA TGG ATT GGA GCT GGT CCA ACA AGT GTC AAA GTT GCA GGG	1897
576 Gly Leu Gln Thr Ala Gly Ala Phe Tyr Glu Trp Ile Gly Ala Gly Pro Thr Ser Val Lys Val Ala Gly	598
1898 TTC AAG ACT GGC ACT ATG GAC TTG ACT GCG TCT GCT TGG ACC TAT AAG ATT GGA TTG CAA GGA GAA CAT	1966
599 Phe Lys Thr Gly Thr Met Asp Leu Thr Ala Ser Ala Trp Thr Tyr Lys Ile Gly Leu Gln Gly Glu His	621
1967 TTG AGG ATA CAG AAG TCA TAT AAC TTG AAG AGT AAA ATT TGG GCA CCA ACT TCG CAG CCA CCA AAG CAA	2035
622 Leu Arg Ile Gln Lys Ser Tyr Asn Leu Lys Ser Lys Ile Trp Ala Pro Thr Ser Gln Pro Pro Lys Gln	644
2036 CAG CCC CTC ACA TGG TAT AAG GCA GTA GTA GAT GCG CCT CCT GGT AAT GAA CCT GTT GCA CTT GAT ATG	2104
645 Gln Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Met	667
2105 ATT CAT ATG GGA AAA GGA ATG GCT TGG TTG AAT GGA CAA GAA ATT GGC AGA TAT TGG CCG AGG AGA ACT	2173
668 Ile His Met Gly Lys Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg Arg Thr	690
2174 TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT	2242
691 Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr	713
2243 GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC	2311
714 Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val	736
2312 TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA	2380
737 Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly	759
2381 GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG	2449
760 Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu	782
2450 AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT ATT TCC TCT GTC AAA TTT	2518
783 Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe	805
2519 GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGC TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT	2587
806 Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser	828
2588 GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT	2656
829 Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe	851
2657 AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCC	2728
852 Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ***	871
2729 AAAATGAATGACATATTTCTAATTATATAGTTTGTCTACGAGATGCTCATTTCTTAAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT	2820
2821 CTTTGGTCTATGATTGAAGTTTAAGATATGAGTACTGATGTCTTATTAAGCATCACCAGATAACCTTTGGATATTCAATGTTTGAAGACTAA	2912
2913 GTATTTCATATTATTTCAGTCGAGATGCAAGATTTATTTGTGAAAAA	2972

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DNASIS
Multiple Edit1Figure 3
Sheet 1 of 4

		10	20	30	40	50	
TBG1-ORF	-24	MGFWMA	MLMLLLCLW	VSCGISVSVYD	26
TBG2-ORF	-14	MSRRKT	LNFPILITVL	TIHFVIVAGE	YFKPENVTYD	36
TBG3-ORF	-20	MGCTLHMLN	VLLVILGWSV	FSGTASVSYD	30
TBG4-ORF	-22	MLRINVL	LIVICHLDFE	SSVKASVSYD	28
TBG5-ORF	1	-----	-----	-----	-----	-----	50
TBG6-ORF	1	-----	-----	-----	-----	-----	50
TBG7-ORF	-1	MNIMSCLSS	NFKFVFLAST	VIWTVMSSS	LAAVDASNT	TIGTDSVTYD	49
apple	-21	MGVGIQTMW	SILLLFSCIF	SAASASVSYD	29
carnation	-16	MLCG	KENNVMQML	VYVFLITLI	SCVYGNWYD	34
asparagus	-20	MAKIVLMIM	VALLAAVWSP	PATVTSVTYD	30
broccoli	-20	MMKQFNLS	LFLITTSFG	SANSTIVSHD	30
Lupin	-12	MEGSRIVM	ESIMSRRNPH	MVLLILFFWV	CYVTSVTYD	38
		60	70	80	90	100	
TBG1-ORF	27	HKATLVNGOR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	76
TBG2-ORF	37	NRALFICGR	RMHSAGHY	BRAEDMWP	ETARSKEGA	DVETTSVYD	86
TBG3-ORF	31	HRAITVNGOR	KILLTSSSVHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	80
TBG4-ORF	29	DRATLNGKR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	78
TBG5-ORF	51	-----	-----	-----	-----	-----	100
TBG6-ORF	51	-----	-----	-----	-----	-----	100
TBG7-ORF	50	RSLTIVNGOR	KLETCASSTHY	PRSVFAMWP	ETRLAKEGGV	DVETTSVYD	99
apple	30	HKATLVNGOR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	79
carnation	35	YRAKINDOR	RMHSAGHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	84
asparagus	31	HKSVLVNGOR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	80
broccoli	31	ERATLIDGOR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	80
Lupin	39	HKATLVNGOR	KILLTSSSTHY	PRSTPEMWP	ETOKAKEGGV	DVETTSVYD	88
		110	120	130	140	150	
TBG1-ORF	77	GHEPSEGKYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	126
TBG2-ORF	87	GHEPTRGOYN	EGGRFDMWE	AKETGSHGIF	LFTIGGFAO	AEWNRGGFPV	136
TBG3-ORF	81	GHEPDOGMAY	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	130
TBG4-ORF	79	GHEPSPGKAN	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	128
TBG5-ORF	101	LHEPVRNQYD	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	150
TBG6-ORF	101	VHEPFGNYN	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	150
TBG7-ORF	100	GHEPSPGNYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	149
apple	80	GHEPSPGNYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	129
carnation	85	GHEPSEGKYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	134
asparagus	81	GHEPSPGQYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	130
broccoli	81	AHEPSPRQYD	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	130
Lupin	89	GHEPSPGKYV	EGGRFDMWE	ETVTEGAGLY	VHLRIGPFAC	AEWNRGGFPV	138
		160	170	180	190	200	
TBG1-ORF	127	WLKYVPGISF	RTDNEPFKAA	MQKETEKIVD	MMK-----AE	KLYETQGGPI	176
TBG2-ORF	137	WLRIIPGIEF	RTDNEPFKAA	MERYVVKIVD	LMK-----SE	SLFESQGGPI	186
TBG3-ORF	131	WLKYVPGISF	RTDNEPFKAA	MQKETEKIVD	MMK-----AE	KLYETQGGPI	180
TBG4-ORF	129	WLKYVPGMEF	RTDNEPFKAA	MQKETEKIVD	MMK-----SE	NLFESQGGPI	178
TBG5-ORF	151	WLHPIPGIEF	RTDNEPFKAA	MQKETEKIVD	MIK-----QE	NLYASQGGPV	200
TBG6-ORF	151	WLKYVPGISF	RTDNEPFKAA	MQKETEKIVD	LMKIIIFSSL	RVVQSYSHRL	200
TBG7-ORF	150	WLHYVPGTTF	RTDNEPFKAA	MQKETEKIVD	LMK-----RE	RLFASQGGPI	199
apple	130	WLKYVPGIAF	RTDNEPFKAA	MQKETEKIVD	MMK-----AE	KLFQTOGGPI	179
carnation	135	WLKYVPGIEF	RTDNEPFKAA	MQKETEKIVD	MMK-----AE	KLFHWQGGPI	184
asparagus	131	WLKYVPGIHF	RTDNEPFKAA	MQKETEKIVD	MMK-----AE	GLYETQGGPI	180
broccoli	131	WLHNPDMKF	RTDNEPFKAA	MQKETEKIVD	MMK-----EE	SLFASQGGPI	180
Lupin	139	WLKYVPGIAF	RTDNEPFKAA	MQKETEKIVD	IMK-----AE	KLFQSQGGPI	188
		210	220	230	240	250	
TBG1-ORF	177	ILSQ-IENEY	GP--MEWELG	EPGKVYSEWA	AKMAVDLGTG	VPWIMCKQD-	226
TBG2-ORF	187	ILSQ-IENEY	GN--VESSFG	PKGKLYMKWA	AEMAVGLGAG	VPWIMCRQ-T	236
TBG3-ORF	181	ILSQ-IENEY	GP--MEWELG	APGKSYAQWA	AKMAVGLDTG	VPWIMCKQD-	230
TBG4-ORF	179	IMAQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLKTG	VPWIMCKQE-	228
TBG5-ORF	201	ILSQ-IENEY	GNGDIESRYG	PRAKPYVNW	ASMATSLNTG	VPWIMCQ-Q	250
TBG6-ORF	201	RMSMGLKPRY	----LEHRDI	SIQHLQIWIQ	----LDLNTG	VPWIMCKEE-	250
TBG7-ORF	200	ILSQ-VENEY	G--YYENAYG	EGGKRYALWA	AKMALSONTG	VPWIMC-QQY	249
apple	180	ILSQ-IENEF	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWIMCKQE-	229
carnation	185	ILNQ-IENEY	GP--VEWEIG	APGKAYTHWA	AQMAQSLNAG	VPWIMCKQDS	234

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asparagus	181	ATCG TENEY	GP--VEYDYG	AAGKSYINWA	AKMAYGNYNS	VSVMKQSD	230	
broccoli	181	ATCG TENEY	GN--VISSYG	AEGKAYIDWC	ANMANSDOTS	VSVMKQSD	230	
Lupin	189	ATCG TENEY	GP--VEWEIG	APGKAYTKWA	AGMAVGLOAS	VSVMKQSD	238	
		260	270	280	290	300		
TBG1-ORF	227	IVFDP INTG	NGFYCDYFTP	NKANKPKMWT	EWATAWRELE	SEVVPKPAE	276	
TBG2-ORF	237	DAPEY IDTC	NAYYDGGFTP	NSEKPKKIWT	ENANGWFADW	GERLPKRPSE	286	
TBG3-ORF	231	DAPDP INAC	NGFYCDYFSP	NKAYKPKIWT	EWATAWRELE	GNVVPKPAE	280	
TBG4-ORF	229	DAPDP VIDTC	NGFYCEGFRP	NKPKPKMWT	EWATAWRELE	GERLPKPAE	278	
TBG5-ORF	251	DAPPS VINTC	NGFYCDQFKQ	NSDKTPKMWT	ENWIGWELSE	SEVVPKPAE	300	
TBG6-ORF	251	DAPDP VINTC	NGFYCDNFPF	NKPKPKIWT	EWATAWRELE	GERLPKPAE	300	
TBG7-ORF	250	DAPDP VIDTC	NSFYCDQFKP	ISANKPKIWT	EWATAWRELE	GARDPKPAE	299	
apple	230	DAPDP VIDTC	NGFYCDNFPF	NKDKPKMWT	EWATAWRELE	SEVVPKPAE	279	
carnation	235	IVFDP NVIDTC	NGFYCEGFRP	KDKSKPKMWT	EWATAWRELE	SEVVPKPAE	284	
asparagus	231	DAPDP VINTC	NGFYCDYFSP	NKDKPKMWT	EWATAWRELE	SEVVPKPAE	280	
broccoli	231	HAPDP MIETG	NGFYCDQFKQ	SNESPKMWT	EWATAWRELE	SEVVPKPAE	280	
Lupin	239	DAPDP IDTC	NGFYCDNFPF	NKDKPKMWT	EWATAWRELE	SEVVPKPAE	288	
		310	320	330	340	350		
TBG1-ORF	277	EMAF AVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	326	
TBG2-ORF	287	EMAF AIAREF	OTGGSLQNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	336	
TBG3-ORF	281	EMAF SVAKRF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	330	
TBG4-ORF	279	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	328	
TBG5-ORF	301	EMAF AVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	350	
TBG6-ORF	301	EMAF AVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	350	
TBG7-ORF	300	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	349	
apple	280	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	329	
carnation	285	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	334	
asparagus	281	EMAF AVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	330	
broccoli	281	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	330	
Lupin	289	EMAF SVAREF	OTGGSKINNY	MYHGGTNEGR	TSCEPKNY	MYHGGTNEGR	338	
		360	370	380	390	400		
TBG1-ORF	327	GSN OPKWGH	LKDLHRAIKL	CEPALVSSD	AVATLASHOC	BAVFKSKA	376	
TBG2-ORF	337	GSN OPKWGH	LKDLHRAIKL	CEPALVSSD	AVATLASHOC	BAVFKSKA	386	
TBG3-ORF	331	GSN OPKWGH	LKDLHRAIKL	CEPALVSSD	AVATLASHOC	BAVFKSKA	380	
TBG4-ORF	329	GLNE PKWGH	LKDLHRAIKL	SEPALVSSY	AAVTSIGSNQ	BAVFKSKA	378	
TBG5-ORF	351	-----	-----	-----	-----	-----	400	
TBG6-ORF	351	-----	-----	-----	-----	-----	400	
TBG7-ORF	350	GLP REP KWGH	LKDLHRAIKS	CEPALVSSD	AVATLASHOC	BAVFKSKA	399	
apple	330	GLP REP KWGH	LKDLHRAIKS	CEPALVSSD	AVATLASHOC	BAVFKSKA	379	
carnation	335	GLP REP KYTH	LKDLHRAIKM	CEPALVSSD	AVATLASHOC	BAVFKSKA	384	
asparagus	331	GLN OPKWGH	LKDLHRAIKL	CEPALVSSD	AVATLASHOC	BAVFKSKA	380	
broccoli	331	GLN OPKWGH	LKDLHRAIKL	CEPALVSSD	AVATLASHOC	BAVFKSKA	380	
Lupin	339	GLNE PKWGH	LKDLHRAIKQ	CEPALVSSD	AVATLASHOC	BAVFKSKA	388	
		410	420	430	440	450		
TBG1-ORF	377	-----	GACAAFLANY	NQHSFAKVAF	GNMHNLPW	SISILPDCKN	426	
TBG2-ORF	387	-----	GICAAFLANI	DEHESATVKF	YGQEPFLPPW	SVVF---CQI	436	
TBG3-ORF	381	-----	GSCAAFLANY	DQHSFATVVF	ANRHNLPW	SISILPDCKN	430	
TBG4-ORF	379	-----	GACAAFLSNY	DSRYSVKVTF	QNRPNLPW	SISILPDCKT	428	
TBG5-ORF	401	-----	-----	-----	-----	-----	450	
TBG6-ORF	401	-----	-----	-----	-----	-----	450	
TBG7-ORF	400	-----	GACAAFLANM	DDKNDKVQF	RHVSYHLPW	SVSILPDCKN	449	
apple	380	-----	D-CAAF LANY	DAKYSVKVSF	GGGQYDLPPW	SISILPDCKT	429	
carnation	385	-----	GSCAAFLANY	DPKWSVKVTF	SGMEFELPAW	SISILPDCKK	434	
asparagus	381	-----	-SCAAFLANF	NSRYATVTF	NGMHNLPW	SVSILPDCKT	430	
broccoli	381	-----	S-----	-FTGNV	NATADALVNF	KGKDYNVPW	SVSILPDCKT	430
Lupin	389	-----	A-CAAF LANY	NTDYSTQVKF	GNGQYDLPPW	SISILPDCKT	438	
		460	470	480	490	500		
TBG1-ORF	427	TVYNTARVGA	QSAQM--K--	-----	-----MTP	VSRGFS--WE	476	
TBG2-ORF	437	AEIQLSTQLR	WGHKLQSKQW	AQILFQLGII	LCFYKLSLKA	SSESFSQSWM	486	
TBG3-ORF	431	TVFNTARIGA	QSAQM--K--	-----	-----MTP	VSRGLP--WQ	480	
TBG4-ORF	429	AVYNTAQVNS	QSSSI--K--	-----	-----MTP	AGGCLS--WQ	478	
TBG5-ORF	451	-----	-----	-----	-----	-----	500	

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TBG6-ORF	451	-----	-----	-----	-----	500		
TBG7-ORF	450	VAFNTAKVGC	QTSIVNMAP	-----	LD L--HPTASSP	KRDIKSLQWE	499	
apple	430	EVYNTAKVGS	QSSQV--Q--	-----	-----	VHSSEP--Q--	479	
carnation	435	EVYNTAKVNE	PSPKLHSE	-----	-----	VISNLN--Q--	484	
asparagus	431	TVFNTAKVSA	QTTT--K--	-----	-----	MOY LG--GSS--	480	
broccoli	431	EAYNTAKVMT	QTSITTEDS	-----	-----	-C-----D	EPEKLRWTR	480
Lupin	439	EVFNTAKVNS	PRLHR--K--	-----	-----	MTF VNSAFA--Q--	488	
TBG1-ORF	477	S-FNEDAASH	EDD--TSIVVG	LEDDTNTTRD	VSDYLWYMTD	LEIDPTE--G--	526	
TBG2-ORF	487	T-LKEPLGVW	GDKN--EISKG	ILDEHLNVKID	QSDYLWYLR	IYISDDDISP	536	
TBG3-ORF	481	S-FNEETSSY	EDS--SETVVG	LEDDTNTTRD	VSDYLWYSTD	VKIDSRE-KF	530	
TBG4-ORF	479	S-YNEETPTA	DDSDH--TANG	LEDDTNTTRD	VSDYLWYMTN	VNTASNE--G--	528	
TBG5-ORF	501	-----	-----	-----	-----	-----	550	
TBG6-ORF	501	-----	-----	-----	-----	-----	550	
TBG7-ORF	500	V-FKETAGVW	GVAE--EISKG	FVDH--EISKG	ATPGLVNTTS	IPVHAEE--DE	549	
apple	480	S-FIETETSS	DETDH--ILDG	HYEDH--ILDG	TTEDH--ILDG	ITIGSDP--AP	529	
carnation	485	S-YSDEVPTA	DSPGTEREK	HYEDH--ILDG	KSDYLWYMTD	VLDLGNP--G--	534	
asparagus	481	A-YTEDTDL	NDN--EISKG	HYEDH--ILDG	RSDYLWYMTD	VDIAKNE--EK	530	
broccoli	481	PERTOKTIL	KGSGDLIAR	HYEDH--ILDG	RSDYLWYMTD	VLDLGNP--G--	530	
Lupin	489	S-YNEEPASS	SENDEPVGTA	HYEDH--ILDG	RSDYLWYMTD	VLDLGNP--G--	538	
TBG1-ORF	527	LNSGN--WVWL	TVFSACHATH	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	576	
TBG2-ORF	537	WEENDVSPFI	DIDEMRDFVR	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	586	
TBG3-ORF	531	LRGGR--WVWL	TVFSACHATH	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	580	
TBG4-ORF	529	LKNK--DPVL	TVMSACHVLT	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	578	
TBG5-ORF	551	-----	-----	-----	-----	-----	600	
TBG6-ORF	551	-----	-----	-----	-----	-----	600	
TBG7-ORF	550	LRN--RGTAM	FVSKKCHAM	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	599	
apple	530	LKNK--SPIL	TVFSACHATH	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	579	
carnation	535	LKKED--EPWL	TVMSACHVLT	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	584	
asparagus	531	LKTGK--YVYL	TVMSACHVLT	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	580	
broccoli	531	SRNMS--L	RVHSAHVLH	AYVNGKVVGN	OLVRDKFDY	REPKKQVWV	580	
Lupin	539	IKDKK--WVWL	TMSACHVLT	VEVNGAGVLT	VHSLENGRGL	VEVNGAGVLT	588	
TBG1-ORF	577	GVNKISLSLSI	AVGLNVGVTH	FETWNAQVLT	EVSLNGLENG	T---RDLTWQ	626	
TBG2-ORF	587	GYNDILILSE	TVGLQNYGAF	LEKDGAGFKG	QIKNGCKSCG	D---INLITS	636	
TBG3-ORF	581	GVNKISLSLSI	AVGLNVGVTH	FETWNAQVLT	EVSLNGLENG	K---RDLTWQ	630	
TBG4-ORF	579	GINKISLSLSV	SVGLNVGVTH	YDTWNAQVLT	EVSLNGLENG	S---RNLAKQ	628	
TBG5-ORF	601	-----	-----	-----	-----	-----	650	
TBG6-ORF	601	-----	-----	-----	-----	-----	650	
TBG7-ORF	600	GKNEISLSLSM	TVGLQTAGAF	YE-WIGAGPT	SVKVAGFKTG	T---MDLTAS	649	
apple	580	GINKLALLSI	SVGLNVGVTH	FETWNAQVLT	EVSLNGLENG	T---WMSGW	629	
carnation	585	GVNRISLSLSA	VVGLANVGWH	FERYNQVLTG	PVTLGLNEG	T---RDLTWQ	634	
asparagus	581	GSNKISLSLSV	SVGLNVGVTH	FETWNAQVLT	EVSLNGLENG	K---RDLTLQ	630	
broccoli	581	GTNHLALLSV	SVGLQNYGFF	FESGPTGNG	EVKLNGYKGD	ETIEKDLSKH	630	
Lupin	589	GNNKISLSLSV	SVGLANVGTH	FETWNTGVLT	EVTLTGLSSG	T---WDLSKQ	638	
TBG1-ORF	627	KWFYKVGKLG	EALSLHLSLG	SPSVE--WVE	GSLVAQKQPL	SWYKTTFNAP	676	
TBG2-ORF	637	LWTYQVGLRG	EFLEVYDVNS	TESAG--WTE	FPTGTTPSVF	SWYKTKFDAP	686	
TBG3-ORF	631	KWSYKVGLKG	EALSLHLSLG	SSSVE--WVE	GSLVAQKQPL	TWYKSTFNAP	680	
TBG4-ORF	629	KWSYKVGLKG	ESLSLHLSLG	SSSVE--WVR	GSLMAQKQPL	TWYKATFNAP	678	
TBG5-ORF	651	-----	-----	-----	-----	-----	700	
TBG6-ORF	651	-----	-----	-----	-----	-----	700	
TBG7-ORF	650	AWTYKIGLQG	EHLRIQKSYN	LKSKI--WAP	TSQPPKQQPL	TWYKAVVDAP	699	
apple	630	KWTYKTGLKG	EALGLHTVTG	SSSVE--WVE	GPSMAEKQPL	TWYKATFNAP	679	
carnation	635	WYSYKIGTKG	EEQOVVNSGG	SSHVQ--WGP	PAW---KQPL	VWYKTTFDAP	684	
asparagus	631	KWTYQIGLHG	ETLSLHSLTG	SSNVE--WGE	AS---QKQPL	TWYKTTFNAP	680	
broccoli	631	QWDYKIGLNG	FNHKLFSMKS	AGHHHRKWS	EKLPAARM-L	SWYKANFKAP	680	
Lupin	639	KWSYKIGLKG	ESLSLHTEAG	SNSVE--WVQ	GSLVAKKQPL	AWYKTTFSAP	688	
TBG1-ORF	677	DGNEPLALDM	NTMGKGQVWI	NGQSLGRHWP	AYKSS-GSCS	V-CNYTGWFD	726	

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TBG2-ORF	687	GCTDPVALDF	SSMGKGOAWV	NSHHVGRYWT	LVAPN-NGCG	RTCDYRGAH	736
TBG3-ORF	681	AGNDPLALDL	NTMGKGQVWI	NGOSLGRYWP	GYKAS-GNCG	A-CNYAGWFN	730
TBG4-ORF	679	GGNDPLALDM	ASMGKGQIWI	NKEGVGRHWP	GYIAQ-GDCS	K-CSYAGTFN	728
TBG5-ORF	701	-----	-----	-----	-----	-----	750
TBG6-ORF	701	-----	-----	-----	-----	-----	750
TBG7-ORF	700	PGNEFVALDM	IHMKGQMAWL	NKEIGRYWP	RRTSKYENCV	TOCDYRGAH	749
apple	680	PGDAPLALDM	GSMGKGQIWI	NGOSVGRHWP	GYIAR-GSCG	D-CSYAGTYD	729
carnation	685	GGNDPLALDL	GSMGKGQAWI	NGOSIGRHWS	NNIAK-GSCN	DNCNYAGTYT	734
asparagus	681	PGNEFVALDM	NTMGKGQIWI	NGOSIGRYWP	AVKAS-GSCG	S-CDYRGTYN	730
broccoli	681	LKQDPVIVL	NGLKGGEVWI	NGOSIGRYWP	SFNSSDGCT	EEDYRGEYG	730
Lupin	689	AGNDPLALDL	GSMGKGQVWV	NGOSIGRHWP	GNKAR-GNCG	N-CNYAGTYT	738
TBG1-ORF	727	EKKCLTNGGE	GSQRWYHVP	SWLYPTGNLL	V-VFEENGGD	PYGITLVKRE	776
TBG2-ORF	737	SDKCRTHNGE	ITQAWYHI PR	SWLKLNNVL	V-I FEETDKT	PFDISISTRS	786
TBG3-ORF	731	EKKCLTNGGE	ASQRWYHVP	SWLYPTGNLL	V-LFEENGGE	PHGISTAVRE	780
TBG4-ORF	729	EKKCLTNGGO	ESQRWYHVP	SWLSPGNLL	V-VFEENGGN	PHGISTAVRS	778
TBG5-ORF	751	-----	-----	-----	-----	-----	800
TBG6-ORF	751	-----	-----	-----	-----	-----	800
TBG7-ORF	750	PDKCVTNGGO	PTQRWYHVP	SWLPTGNLL	I-I FEETDKT	ESDRFSMRK	799
apple	730	DKKCRTHNGE	PSQRWYHI PR	SWLPTGNLL	V-VFEENGGD	PSRISIVERG	779
carnation	735	EKKCLTNGGE	SSQRWYHVP	SWLPTGNLL	V-VFEENGGD	TKWVSEVIRT	784
asparagus	731	EKKCLTNGGE	ASQRWYHVP	SWLPTGNLL	V-VFEENGGD	PHGISTAVRE	780
broccoli	731	SDKCAFMGSK	PTQRWYHVP	SWLPTGNLL	V-VFEENGGD	PSMVKFKTVV	780
Lupin	739	DTKCLTNGGO	PSQRWYHVP	SWLPTGNLL	V-VFEENGGD	PHGISTAVRT	788
TBG1-ORF	777	IGSVCAEVEE	WG-POLVNW	RLVSKFDRP	IR--PKAHLK	QAPGOKTSS	826
TBG2-ORF	787	TETICAVVSE	KHYPLHKAS	HSEFDRKLSL	MDKTPEMHDO	QDEGHTSSS	836
TBG3-ORF	781	VASVCADINE	WG-POLVNW	MDKSKVLP	IR--PKAHLK	QASGOKTSS	830
TBG4-ORF	779	-----	-----	-----	-----	-----	828
TBG5-ORF	801	-----	-----	-----	-----	-----	850
TBG6-ORF	801	-----	-----	-----	-----	-----	850
TBG7-ORF	800	VSGACGHLV	-DHESFD--V	ENLOGSEIEN	DKNRPTLSLK	CPTININISSV	849
apple	780	-----	-----	-----	TA--AK--	-----	829
carnation	785	IA--	-----	-----	-----	-----	834
asparagus	781	VASVCAEVEE	LQ-PIMDNR	TKVNG--	-R--PRVHLS	QDEGOKMSKI	830
broccoli	781	TGRVCAKAHE	-----	-----	-----	-----	830
Lupin	789	-----	-----	-----	-----	-----	838
TBG1-ORF	827	KFASFGTPEG	VCGNFQOGSC	HAPRSYDAFK	K-----NCVG	KECSQVQVTP	876
TBG2-ORF	837	EFASYGSPNG	SCQKESQKCK	HANSLSV--	---VSQACIG	RTSCSIGISN	886
TBG3-ORF	831	KFASFGTPQG	VCGSFREGSC	HAFHSYDAFE	R-----YCIG	QNSCSVPVTP	880
TBG4-ORF	829	-----	-----	-----	-----	-----	878
TBG5-ORF	851	-----	-----	-----	-----	-----	900
TBG6-ORF	851	-----	-----	-----	-----	-----	900
TBG7-ORF	850	KFASFGNPNQ	TCGSYMLGDC	HDQNSAALVE	K-----VCLN	QNECALEMSS	899
apple	830	-----	-----	-----	-----	-----	879
carnation	835	-----	-----	-----	-----	-----	884
asparagus	831	KFASFGTPQG	TCGSFSEGGC	HAKHSYDAFE	QEGLMQNCVG	QEFCSVNVP	880
broccoli	831	KFASFGNPSG	QCGSFAAGSC	EGAKDAVKV-	---VAKECVG	KLNCMTMVSS	880
Lupin	839	-----	-----	-----	-----	-----	888
TBG1-ORF	877	ENFGGDP-CR	NVLKKLSVEA	ICS-----	-----	-----	926
TBG2-ORF	887	GVFG-DP-CR	HVVKSLAVQA	KCSPPDLST	SASS-----	-----	936
TBG3-ORF	881	EIFGGDP-CP	HVMKKLSVEV	ICS-----	-----	-----	930
TBG4-ORF	879	-----	-----	-----	-----	-----	928
TBG5-ORF	901	-----	-----	-----	-----	-----	950
TBG6-ORF	901	-----	-----	-----	-----	-----	950
TBG7-ORF	900	ANFNMQL-CP	STVKKLAVEV	NCS-----	-----	-----	949
apple	880	-----	-----	-----	-----	-----	929
carnation	885	-----	-----	-----	-----	-----	934
asparagus	881	EVFGGDP-CP	GTMKKLAVEA	ICE-----	-----	-----	930
broccoli	881	HKFGSNLDCG	DSPKRLFVEV	EC-----	-----	-----	930

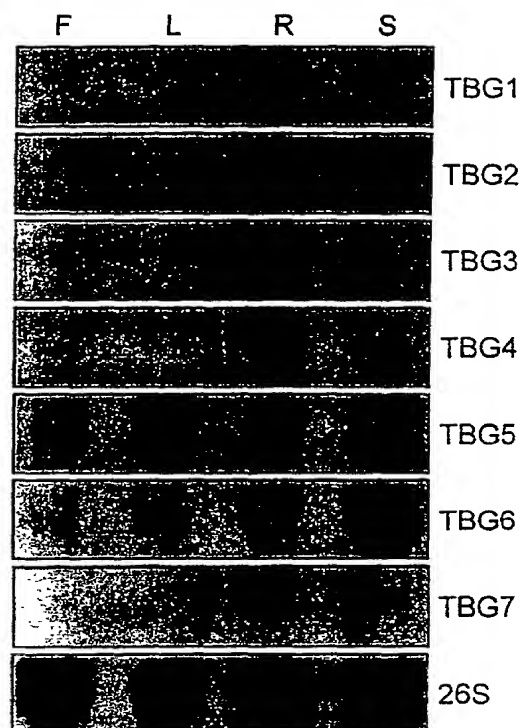


Figure 4. Autoradiograph of northern blot analysis of TBG expression in various plant tissues. Twenty μg of total RNA extracted from flowers (F), leaves (L), roots (R) and stems (S) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown.

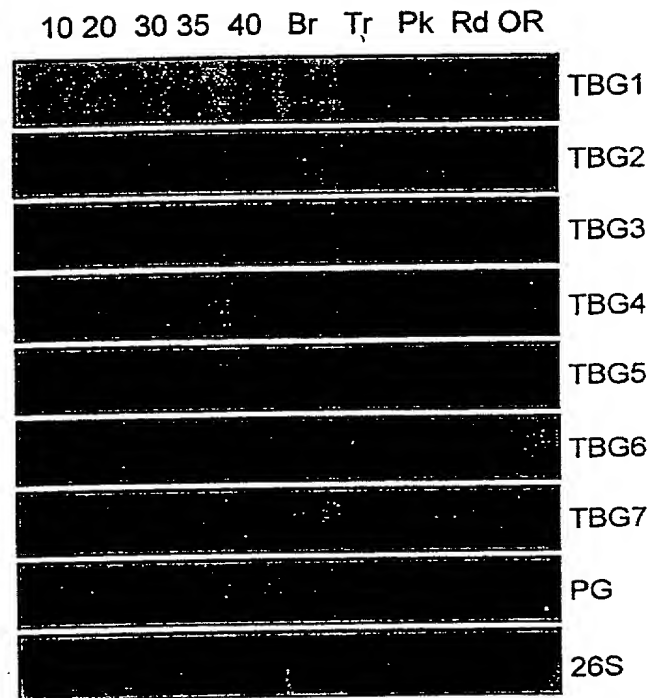


Figure 5. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue was loaded in each lane. Fruit were harvested at 10, 20, 30, 35, and 40 days post-pollination and at the breaker (Br), turning (Tr), pink (Pk), red (Rd) and over ripe (OR) stages. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.



Figure 6. Autoradiograph of northern blot analysis of TBG expression in fruit tissues. Twenty μ g of total RNA extracted from mature green or turning stage fruit peel (P), outer pericarp (OP), inner pericarp (IP) and locular (L) tissue was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.

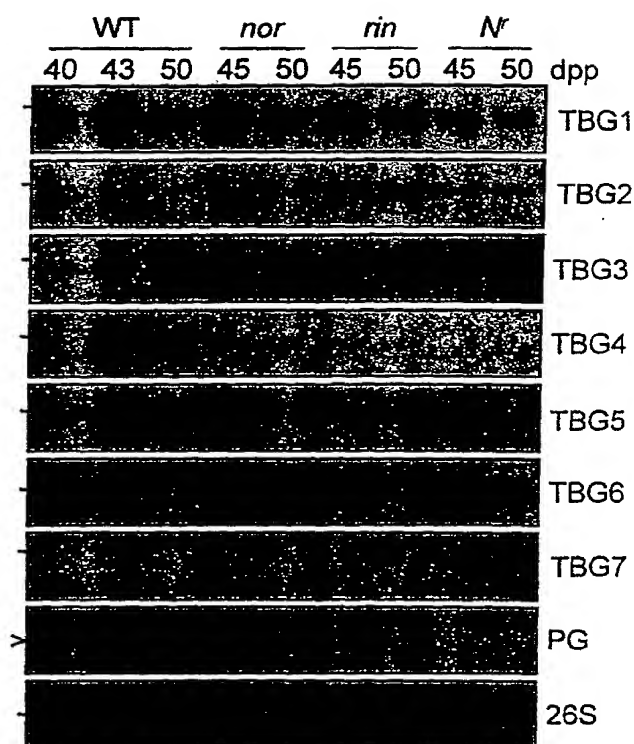


Figure 7. Autoradiograph of northern blot analysis of TBG expression in normal and mutant fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue at various days post-pollination (dpp) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control. The - and + marks on the left indicate the position of the tomato 27S and 18S rRNAs respectively.

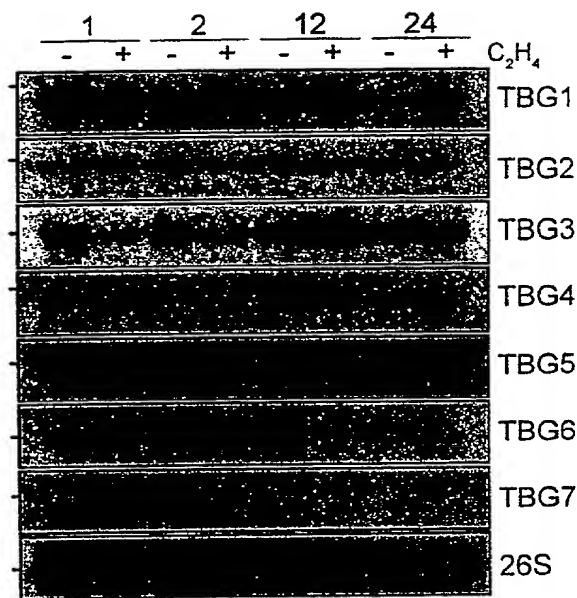


Figure 8. Autoradiograph of northern blot analysis of TBG expression in response to ethylene treatment of mature green fruit tissues. Twenty μ g of total RNA extracted from peel and outer pericarp tissue at various times (1, 2, 12 and 24 hours) after treatment with (+) or without (-) 10 ppm ethylene was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. The - marks on the left indicate the position of the tomato 27S rRNA.

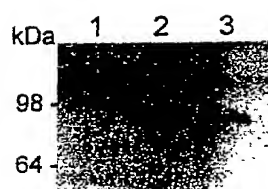


Figure 9. Western blot analysis of TBG4 expression by yeast. A yeast clone was isolated that secreted high levels of FLAG-TBG4 fusion protein into the culture medium. Protein samples were separated in an 8% acrylamide gel, transferred to nitrocellulose and were blotted with M1 anti-FLAG primary antibody. Blots were washed and blotted with an alkaline-phosphatase conjugated secondary antibody and alkaline phosphatase activity was detected using Sigma Fast substrate. Lane 1, culture medium of an untransformed yeast clone was used as a negative control. Lane 2, culture medium of yeast clone expressing FLAG-TBG4 fusion protein. Lane 3, Affinity purified FLAG-TBG4 fusion protein.

Figure 10

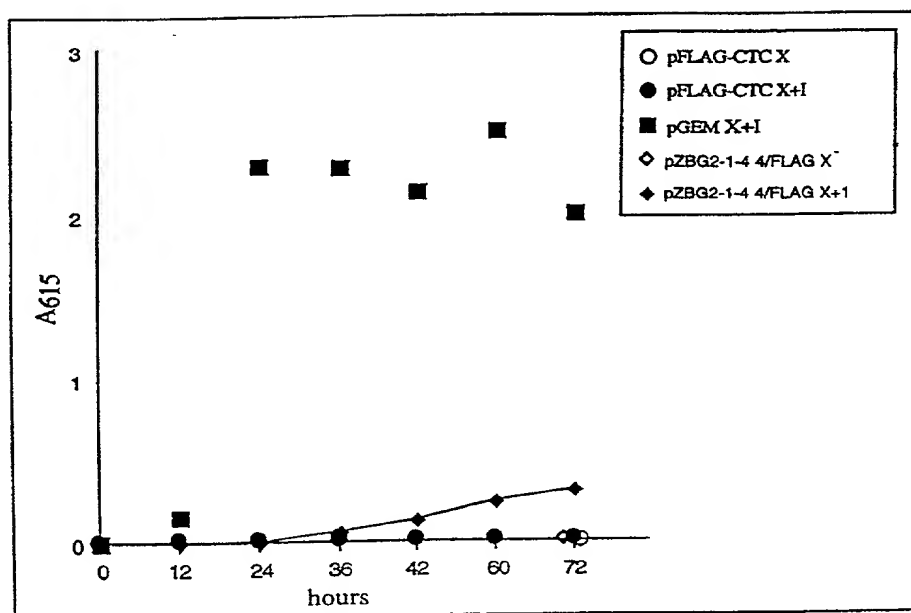
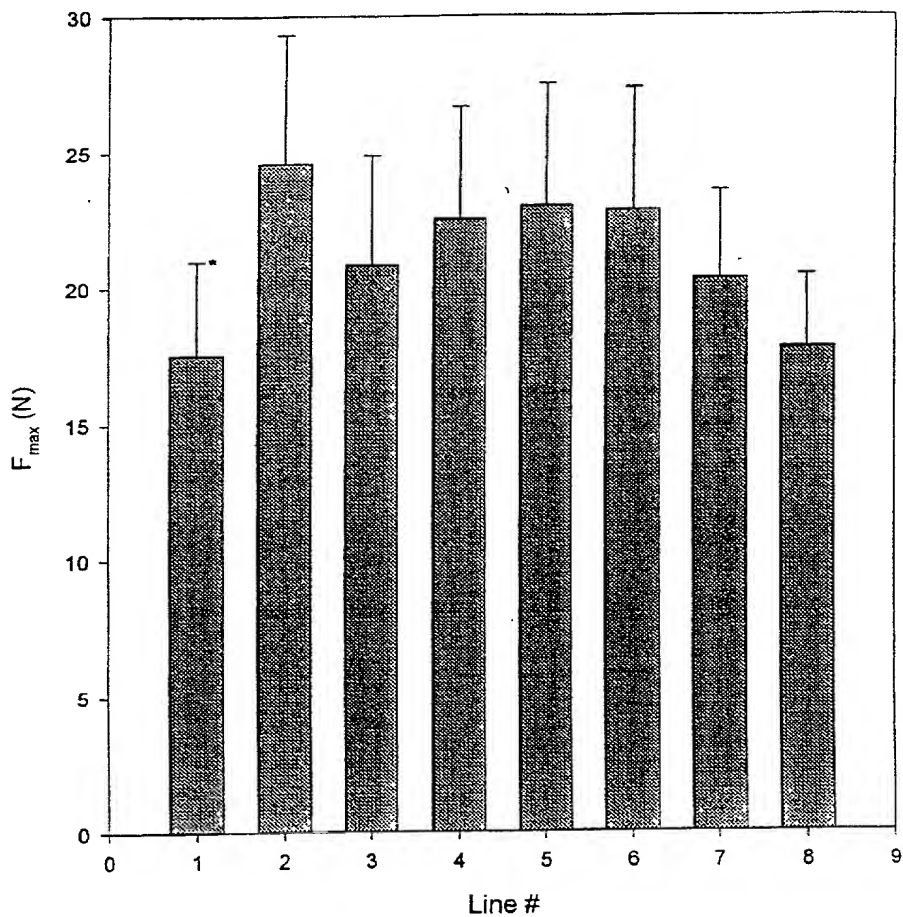


Figure 11A

Flat plate compression to 3 mm
Breaker + 7 d



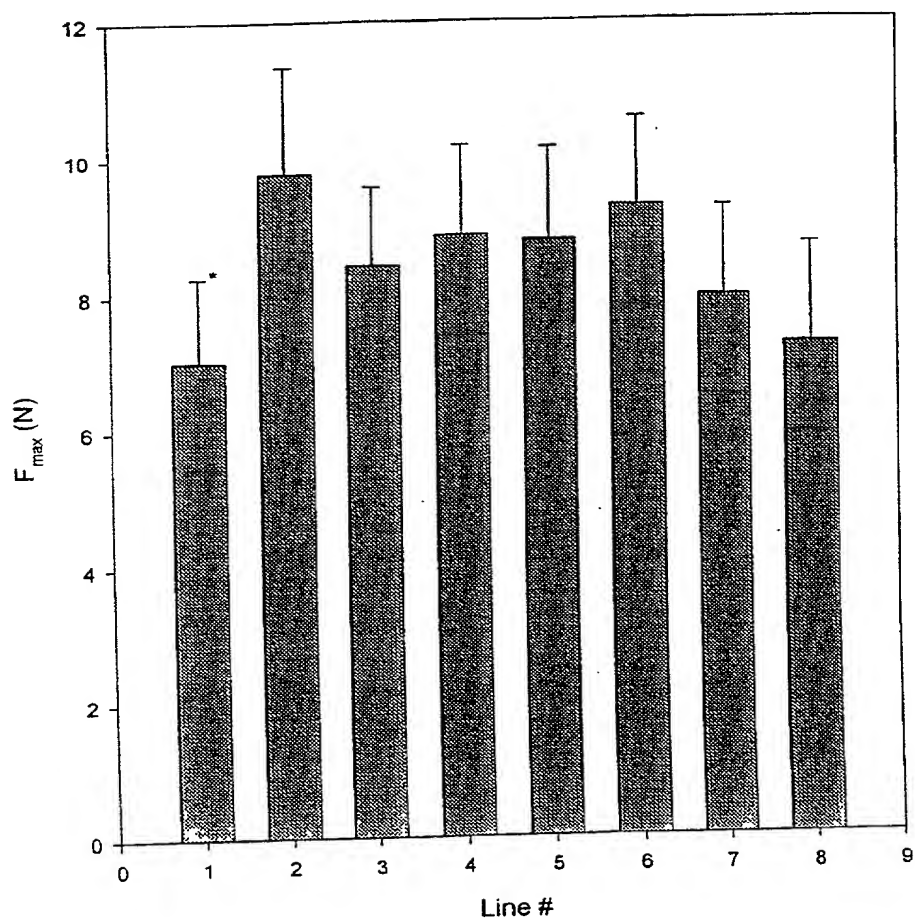
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FP07 Line # FP07 mean FP07 std dev

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5	23.03255	4.493091
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Figure 11B

Spherical indenter to 3 mm
Breaker + 7 d

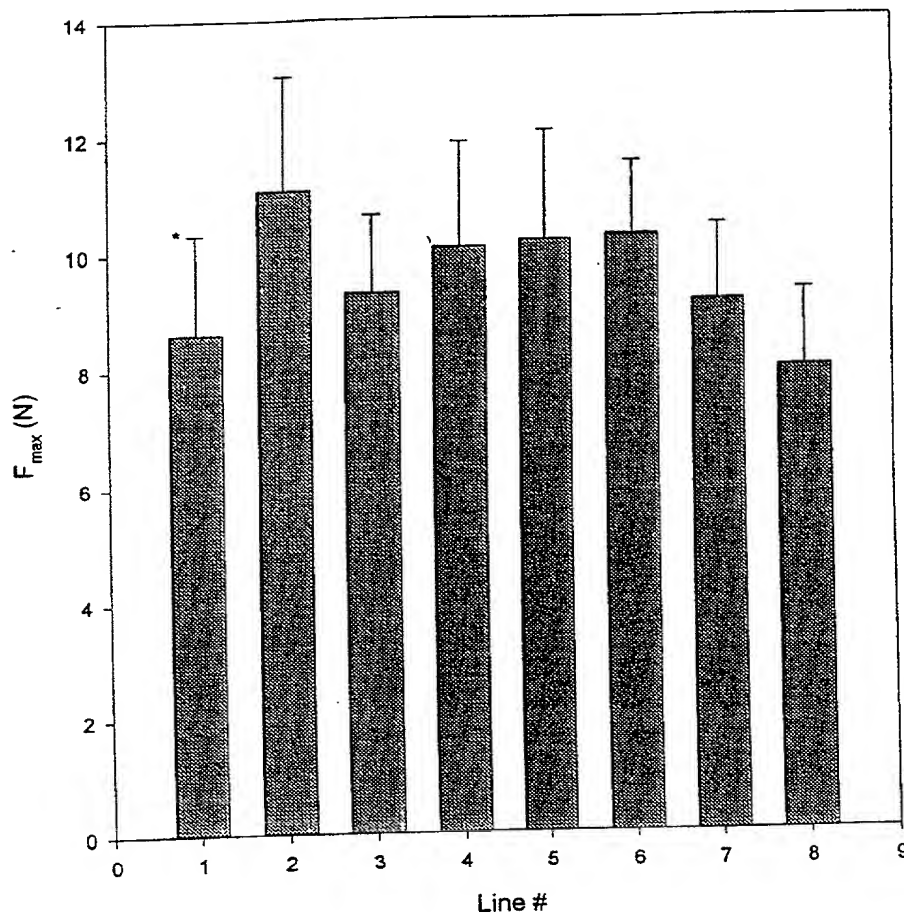


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6	8.43	1.15
7	8.87	1.32
8	8.78	1.36
9	9.28	1.29
11	7.96	1.30
12	7.26	1.45

Figure 11C

4-mm cylindrical indenter to 1 mm
Breaker + 7 d

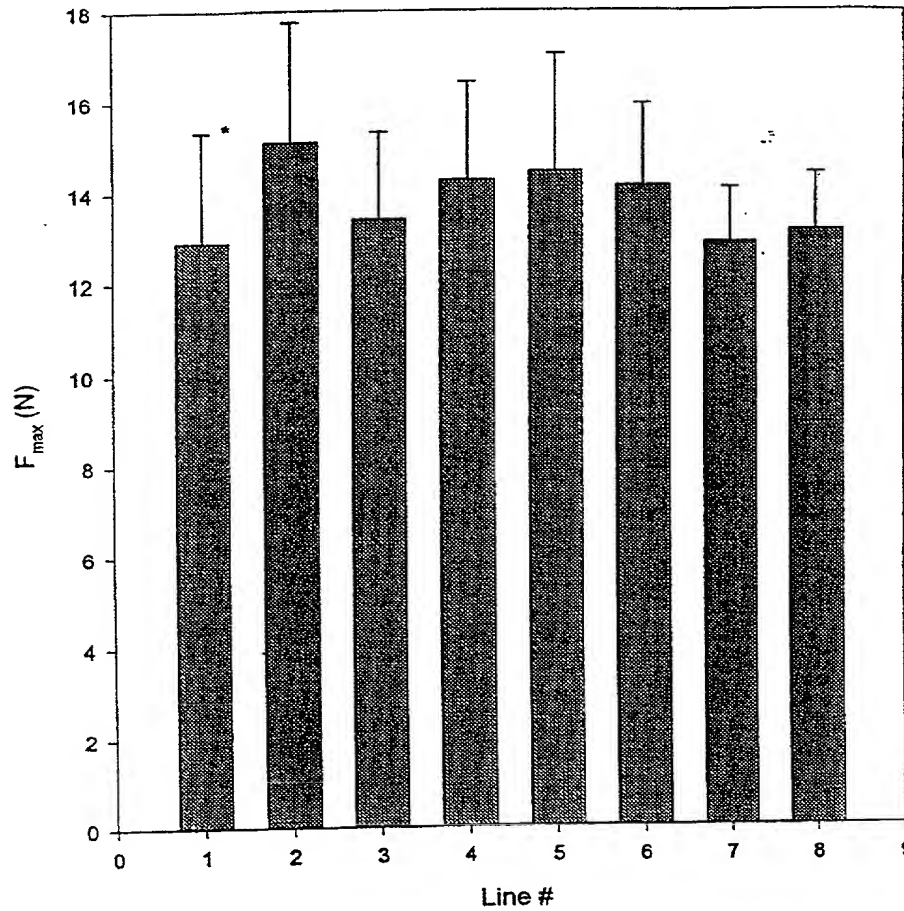


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	8	10.18	1.88
	9	10.27	1.26
	11	9.15	1.30
	12	7.99	1.33

Figure 11D

4-mm cylindrical puncture to 1 mm
Breaker + 7.8



* Standard Deviation

PU07 Line#	PU07 Mean	PU07 Std Dev
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5	15.13	2.61
6	13.44	1.90
7	14.28	2.16
8	14.47	2.58
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FIG. 11 E (1)
Flat plate compression to 3 mm
Breaker + 7 d

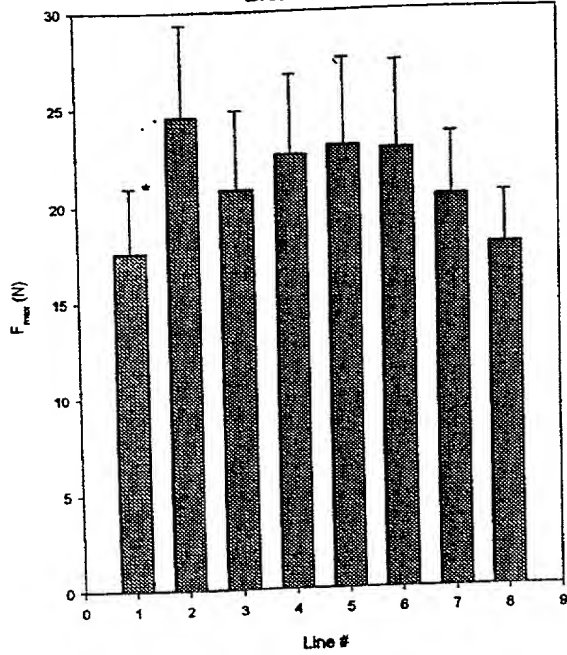


FIG. 11 E (2)
Spherical indenter to 3 mm
Breaker + 7 d

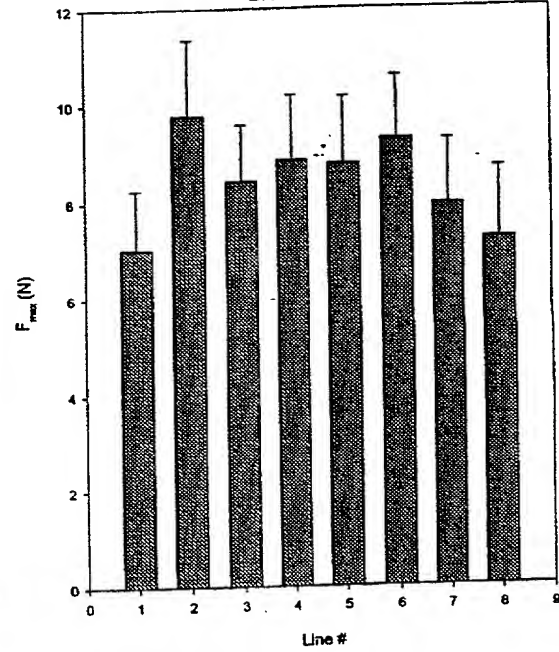


FIG. 11 E (3)
4-mm cylindrical indenter to 3 mm
Breaker + 7 d

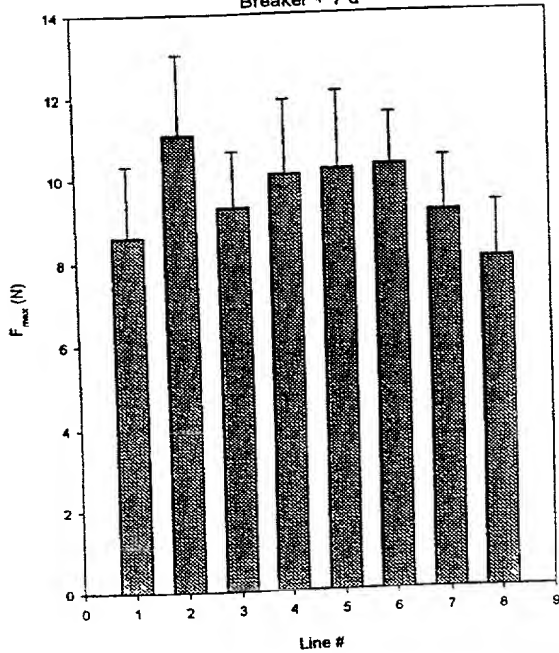
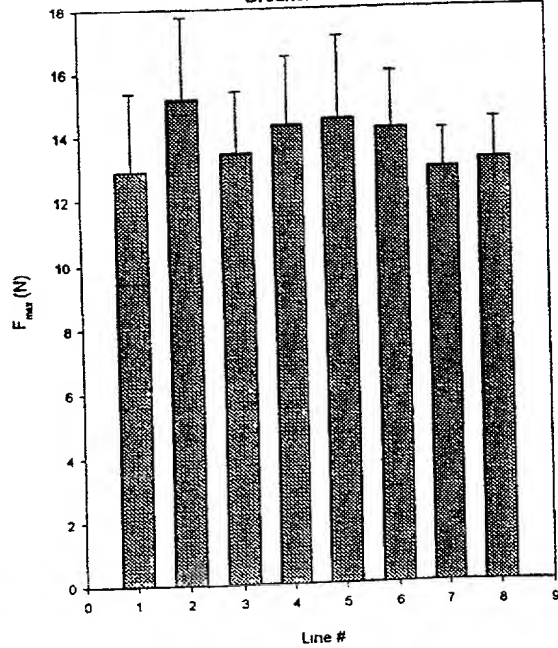


FIG. 11 E (4)
4-mm cylindrical puncture to 10 mm
Breaker + 7 d



* Standard Deviation

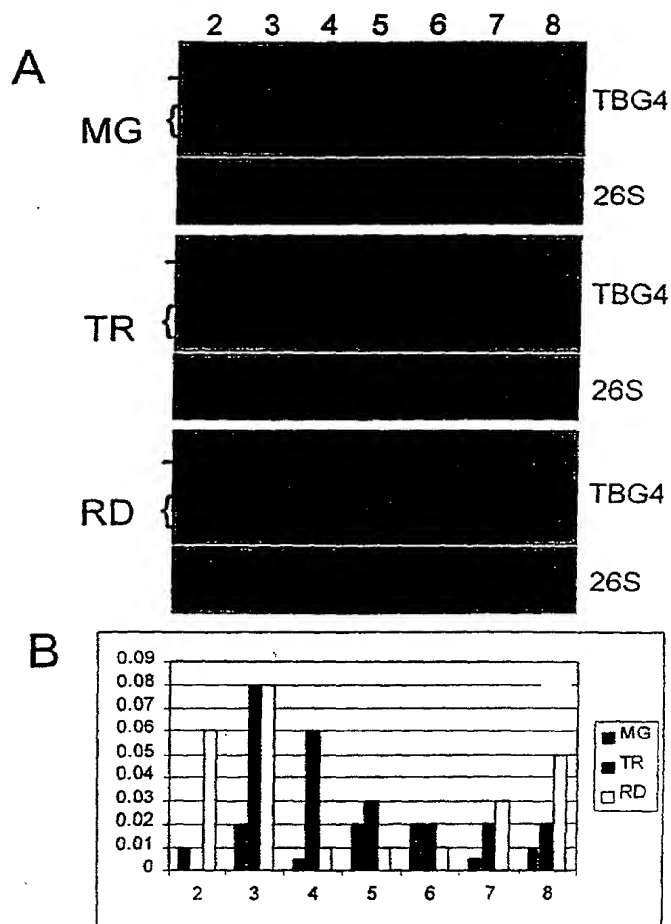


Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct. A. Total RNA was extracted from mature green/42 days post-pollination (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty μ g was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E. B. Chart of TBG4 mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

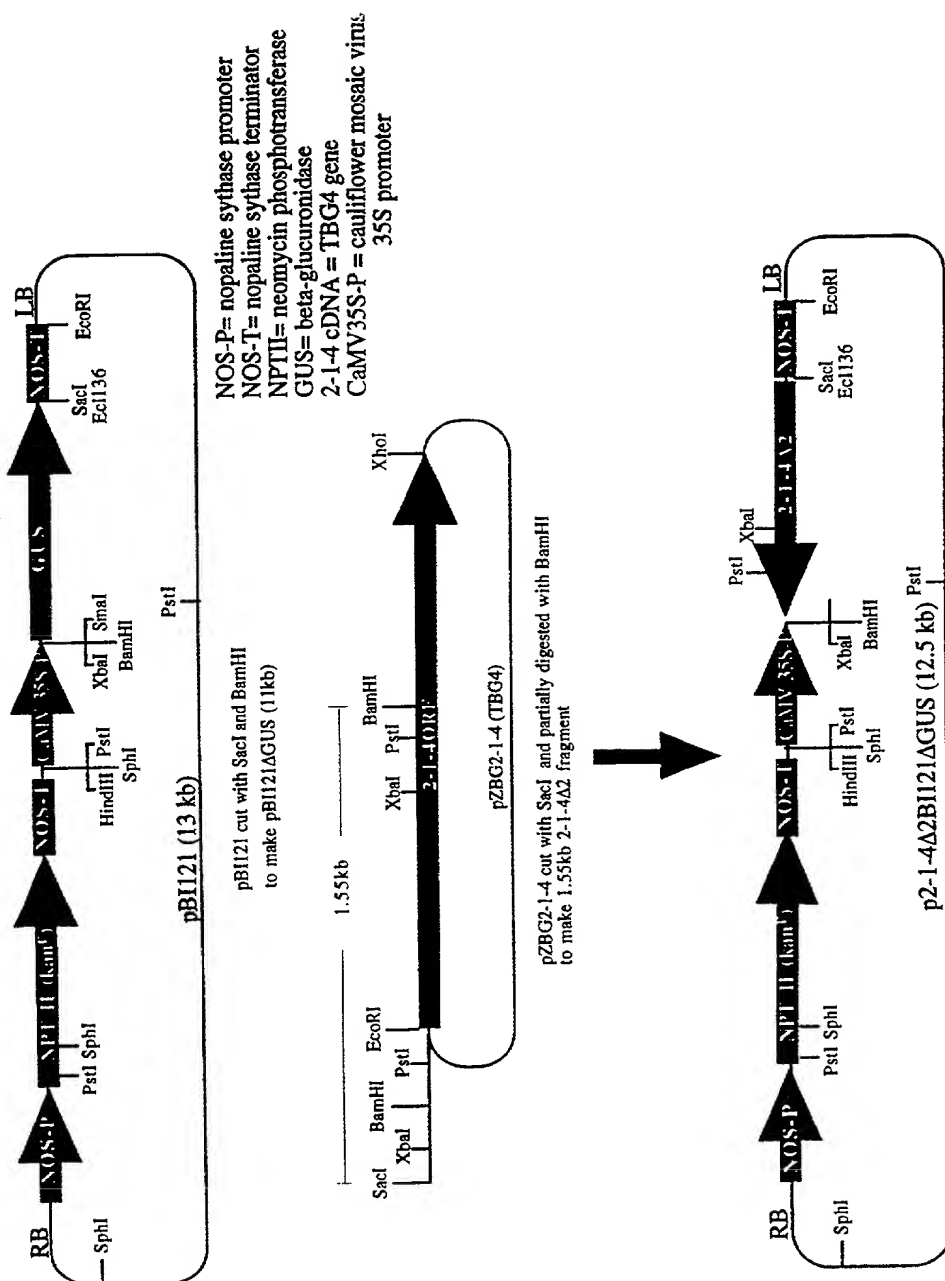


Figure 13. Binary construct used to transform plants and express TBG4 (pZBG2-1-4) in the antisense orientation.

Docket No.
0066.99

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

Genes Coding for Tomato B-Galactosidase Polypeptides

the specification of which

(check one)

☐ is attached hereto.

☒ was filed on June 8, 1999 as United States Application No. or PCT International Application Number PCT/US99/12697

and was amended on _____

(if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Priority Not Claimed

(Number)

(Country)

(Day/Month/Year Filed)

☐

(Number)

(Country)

(Day/Month/Year Filed)

☐

(Number)

(Country)

(Day/Month/Year Filed)

☐

I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

60/088,805

June 9, 1998

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

I hereby claim the benefit under 35 U. S. C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, C. F. R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. (list name and registration number)

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Sole or first inventor's signature	Date
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Second inventor's signature	Date
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SEQUENCE LISTING

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<210> 4

<211> 2554

<212> DNA

<213> Lycopersicon esculentum

<400> 4

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 ttatttggat tatgagattg aagaagattg tacagcttcc aaatactatt agaatacaaa 2520
 taaatttcac gtaaaaaaaaa aaaaaaaaaa aaaa 2554

<210> 5

<211> 755

<212> DNA

<213> *Lycopersicon esculentum*

<400> 5

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 cgattcacag ctaaaattgt tgacatgac aagcaagaaa atctatatgc atcccagggt 300
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 acgggagtg catgggttat gtgtcagcaa ccagatgccc ctcttccgt tattaacact 480
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 gaagacatcg ctttcgtgt ggctcgatt ttccagcgag gcggaactt ccagaactat 660
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<210> 6

<211> 749

<212> DNA

<213> *Lycopersicon esculentum*

<400> 6

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 ttggcatttg ctgttgccca atttatacaa agaggaggat cttttgttaa ctattacatg 660
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<210> 7

<211> 2972

<212> DNA

<213> *Lycopersicon esculentum*

<400> 7

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<210> 8

<211> 835

<212> PRT

<213> *Lycopersicon esculentum*

<400> 8

Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Leu Cys Leu Trp

1 5 10 15

Val Ser Cys Gly Ile Ala Ser Val Ser Tyr Asp His Lys Ala Ile Ile

20 25 30

Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His Tyr Pro

35 40 45

Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu

50 55 60

Gly Gly Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu

65 70 75 80
 Pro Glu Glu Gly Lys Tyr Tyr Phe Glu Glu Arg Tyr Asp Leu Val Lys
 85 90 95
 Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile
 100 105 110
 Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp
 115 120 125
 Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg Thr Asn Asn Glu Pro Phe
 130 135 140
 Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys
 145 150 155 160
 Ala Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln
 165 170 175
 Ile Glu Asn Glu Tyr Gly Pro Met Glu Trp Glu Leu Gly Glu Pro Gly
 180 185 190
 Lys Val Tyr Ser Glu Trp Ala Ala Lys Met Ala Val Asp Leu Gly Thr
 195 200 205
 Gly Val Pro Trp Ile Met Cys Lys Gln Asp Asp Val Pro Asp Pro Ile
 210 215 220
 Ile Asn Thr Cys Asn Gly Phe Tyr Cys Asp Tyr Phe Thr Pro Asn Lys
 225 230 235 240
 Ala Asn Lys Pro Lys Met Trp Thr Glu Ala Trp Thr Ala Trp Phe Thr
 245 250 255
 Glu Phe Gly Gly Pro Val Pro Tyr Arg Pro Ala Glu Asp Met Ala Phe
 260 265 270
 Ala Val Ala Arg Phe Ile Gln Thr Gly Gly Ser Phe Ile Asn Tyr Tyr
 275 280 285
 Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr Ser Gly Gly Pro Phe
 290 295 300
 Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Phe Gly Ser
 305 310 315 320

Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile
325 330 335

Lys Leu Cys Glu Pro Ala Leu Val Ser Val Asp Pro Thr Val Thr Ser
340 345 350

Leu Gly Asn Tyr Gln Glu Ala Arg Val Phe Lys Ser Glu Ser Gly Ala
355 360 365

Cys Ala Ala Phe Leu Ala Asn Tyr Asn Gln His Ser Phe Ala Lys Val
370 375 380

Ala Phe Gly Asn Met His Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile
385 390 395 400

Leu Pro Asp Cys Lys Asn Thr Val Tyr Asn Thr Ala Arg Val Gly Ala
405 410 415

Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Phe Ser Trp
420 425 430

Glu Ser Phe Asn Glu Asp Ala Ala Ser His Glu Asp Asp Thr Phe Thr
435 440 445

Val Val Gly Leu Leu Glu Gln Ile Asn Ile Thr Arg Asp Val Ser Asp
450 455 460

Tyr Leu Trp Tyr Met Thr Asp Ile Glu Ile Asp Pro Thr Glu Gly Phe
465 470 475 480

Leu Asn Ser Gly Asn Trp Pro Trp Leu Thr Val Phe Ser Ala Gly His
485 490 495

Ala Leu His Val Phe Val Asn Gly Gln Leu Ala Gly Thr Val Tyr Gly
500 505 510

Ser Leu Glu Asn Pro Lys Leu Thr Phe Ser Asn Gly Ile Asn Leu Arg
515 520 525

Ala Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val Gly Leu Pro
530 535 540

Asn Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro
545 550 555 560

Val Ser Leu Asn Gly Leu Asn Glu Gly Thr Arg Asp Leu Thr Trp Gln

565 570 575

Lys Trp Phe Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu Ser Leu His
580 585 590

Ser Leu Ser Gly Ser Pro Ser Val Glu Trp Val Glu Gly Ser Leu Val
595 600 605

Ala Gln Lys Gln Pro Leu Ser Trp Tyr Lys Thr Thr Phe Asn Ala Pro
610 615 620

Asp Gly Asn Glu Pro Leu Ala Leu Asp Met Asn Thr Met Gly Lys Gly
625 630 635 640

Gln Val Trp Ile Asn Gly Gln Ser Leu Gly Arg His Trp Pro Ala Tyr
645 650 655

Lys Ser Ser Gly Ser Cys Ser Val Cys Asn Tyr Thr Gly Trp Phe Asp
660 665 670

Glu Lys Lys Cys Leu Thr Asn Cys Gly Glu Gly Ser Gln Arg Trp Tyr
675 680 685

His Val Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu Leu Val Val
690 695 700

Phe Glu Glu Trp Gly Gly Asp Pro Tyr Gly Ile Thr Leu Val Lys Arg
705 710 715 720

Glu Ile Gly Ser Val Cys Ala Asp Ile Tyr Glu Trp Gln Pro Gln Leu
725 730 735

Leu Asn Trp Gln Arg Leu Val Ser Gly Lys Phe Asp Arg Pro Leu Arg
740 745 750

Pro Lys Ala His Leu Lys Cys Ala Pro Gly Gln Lys Ile Ser Ser Ile
755 760 765

Lys Phe Ala Ser Phe Gly Thr Pro Glu Gly Val Cys Gly Asn Phe Gln
770 775 780

Gln Gly Ser Cys His Ala Pro Arg Ser Tyr Asp Ala Phe Lys Lys Asn
785 790 795 800

Cys Val Gly Lys Glu Ser Cys Ser Val Gln Val Thr Pro Glu Asn Phe
805 810 815

Gly Gly Asp Pro Cys Arg Asn Val Leu Lys Lys Leu Ser Val Glu Ala
820 825 830

Ile Cys Ser
835

<210> 9

<211> 887

<212> PRT

<213> Lycopersicon esculentum

<400> 9

Ser Arg Arg Lys Thr Leu Asn Phe Pro Leu Ile Leu Thr Val Leu Thr
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Ile His Phe Val Ile Val Ala Gly Glu Tyr Phe Lys Pro Phe Asn Val
20 25 30

Thr Tyr Asp Asn Arg Ala Leu Ile Ile Gly Gly Lys Arg Arg Met Leu
35 40 45

Ile Ser Ala Gly Ile His Tyr Pro Arg Ala Thr Pro Glu Met Trp Pro
50 55 60

Thr Leu Ile Ala Arg Ser Lys Glu Gly Gly Ala Asp Val Ile Glu Thr
65 70 75 80

Tyr Thr Phe Trp Asn Gly His Glu Pro Thr Arg Gly Gln Tyr Asn Phe
85 90 95

Glu Gly Arg Tyr Asp Ile Val Lys Phe Ala Lys Leu Val Gly Ser His
100 105 110

Gly Leu Phe Leu Phe Ile Arg Ile Gly Pro Tyr Ala Cys Ala Glu Trp
115 120 125

Asn Phe Gly Gly Phe Pro Ile Trp Leu Arg Asp Ile Pro Gly Ile Glu
130 135 140

Phe Arg Thr Asp Asn Ala Pro Phe Lys Glu Glu Met Glu Arg Tyr Val
145 150 155 160

Lys Lys Ile Val Asp Leu Met Ile Ser Glu Ser Leu Phe Ser Trp Gln
165 170 175

Gly Gly Pro Ile Ile Leu Leu Gln Ile Glu Asn Glu Tyr Gly Asn Val
180 185 190

Glu Ser Ser Phe Gly Pro Lys Gly Lys Leu Tyr Met Lys Trp Ala Ala
195 200 205

Glu Met Ala Val Gly Leu Gly Ala Gly Val Pro Trp Val Met Cys Arg
210 215 220

Gln Thr Asp Ala Pro Glu Tyr Ile Ile Asp Thr Cys Asn Ala Tyr Tyr
225 230 235 240

Cys Asp Gly Phe Thr Pro Asn Ser Glu Lys Lys Pro Lys Ile Trp Thr
245 250 255

Glu Asn Trp Asn Gly Trp Phe Ala Asp Trp Gly Glu Arg Leu Pro Tyr
260 265 270

Arg Pro Ser Glu Asp Ile Ala Phe Ala Ile Ala Arg Phe Phe Gln Arg
275 280 285

Gly Gly Ser Leu Gln Asn Tyr Tyr Met Tyr Phe Gly Gly Thr Asn Phe
290 295 300

Gly Arg Thr Ala Gly Gly Pro Thr Gln Ile Thr Ser Tyr Asp Tyr Asp
305 310 315 320

Ala Pro Leu Asp Glu Tyr Gly Leu Leu Arg Gln Pro Lys Trp Gly His
325 330 335

Leu Lys Asp Leu His Ala Ala Ile Lys Leu Cys Glu Pro Ala Leu Val
340 345 350

Ala Ala Asp Ser Pro Gln Tyr Ile Lys Leu Gly Pro Lys Gln Glu Ala
355 360 365

His Val Tyr Arg Gly Thr Ser Asn Asn Ile Gly Gln Tyr Met Ser Leu
370 375 380

Asn Glu Gly Ile Cys Ala Ala Phe Ile Ala Asn Ile Asp Glu His Glu
385 390 395 400

Ser Ala Thr Val Lys Phe Tyr Gly Gln Glu Phe Thr Leu Pro Pro Trp
405 410 415

Ser Val Val Phe Cys Gln Ile Ala Glu Ile Gln Leu Ser Thr Gln Leu

420 425 430
Arg Trp Gly His Lys Leu Gln Ser Lys Gln Trp Ala Gln Ile Leu Phe
435 440 445

Gln Leu Gly Ile Ile Leu Cys Phe Tyr Lys Leu Ser Leu Lys Ala Ser
450 455 460

Ser Glu Ser Phe Ser Gln Ser Trp Met Thr Leu Lys Glu Pro Leu Gly
465 470 475 480

Val Trp Gly Asp Lys Asn Phe Thr Ser Lys Gly Ile Leu Glu His Leu
485 490 495

Asn Val Thr Lys Asp Gln Ser Asp Tyr Leu Trp Tyr Leu Thr Arg Ile
500 505 510

Tyr Ile Ser Asp Asp Asp Ile Ser Phe Trp Glu Glu Asn Asp Val Ser
515 520 525

Pro Thr Ile Asp Ile Asp Ser Met Arg Asp Phe Val Arg Ile Phe Val
530 535 540

Asn Gly Gln Leu Ala Gly Ser Val Lys Gly Lys Trp Ile Lys Val Val
545 550 555 560

Gln Pro Val Lys Leu Val Gln Gly Tyr Asn Asp Ile Leu Leu Leu Ser
565 570 575

Glu Thr Val Gly Leu Gln Asn Tyr Gly Ala Phe Leu Glu Lys Asp Gly
580 585 590

Ala Gly Phe Lys Gly Gln Ile Lys Leu Thr Gly Cys Lys Ser Gly Asp
595 600 605

Ile Asn Leu Thr Thr Ser Leu Trp Thr Tyr Gln Val Gly Leu Arg Gly
610 615 620

Glu Phe Leu Glu Val Tyr Asp Val Asn Ser Thr Glu Ser Ala Gly Trp
625 630 635 640

Thr Glu Phe Pro Thr Gly Thr Thr Pro Ser Val Phe Ser Trp Tyr Lys
645 650 655

Thr Lys Phe Asp Ala Pro Gly Gly Thr Asp Pro Val Ala Leu Asp Phe
660 665 670

Ser Ser Met Gly Lys Gly Gln Ala Trp Val Asn Gly His His Val Gly
675 680 685

Arg Tyr Trp Thr Leu Val Ala Pro Asn Asn Gly Cys Gly Arg Thr Cys
690 695 700

Asp Tyr Arg Gly Ala Tyr His Ser Asp Lys Cys Arg Thr Asn Cys Gly
705 710 715 720

Glu Ile Thr Gln Ala Trp Tyr His Ile Pro Arg Ser Trp Leu Lys Thr
725 730 735

Leu Asn Asn Val Leu Val Ile Phe Glu Glu Thr Asp Lys Thr Pro Phe
740 745 750

Asp Ile Ser Ile Ser Thr Arg Ser Thr Glu Thr Ile Cys Ala Gln Val
755 760 765

Ser Glu Lys His Tyr Pro Pro Leu His Lys Trp Ser His Ser Glu Phe
770 775 780

Asp Arg Lys Leu Ser Leu Met Asp Lys Thr Pro Glu Met His Leu Gln
785 790 795 800

Cys Asp Glu Gly His Thr Ile Ser Ser Ile Glu Phe Ala Ser Tyr Gly
805 810 815

Ser Pro Asn Gly Ser Cys Gln Lys Phe Ser Gln Gly Lys Cys His Ala
820 825 830

Ala Asn Ser Leu Ser Val Val Ser Gln Ala Cys Ile Gly Arg Thr Ser
835 840 845

Cys Ser Ile Gly Ile Ser Asn Gly Val Phe Gly Asp Pro Cys Arg His
850 855 860

Val Val Lys Ser Leu Ala Val Gln Ala Lys Cys Ser Pro Pro Pro Asp
865 870 875 880

Leu Ser Thr Ser Ala Ser Ser
885

<210> 10

<211> 838

<212> PRT

<213> Lycopersicon esculentum

<400> 10

Met Gly Cys Thr Leu Ile Leu Met Leu Asn Val Leu Leu Val Leu Leu

1 5 10 15

Gly Ser Trp Val Phe Ser Gly Thr Ala Ser Val Ser Tyr Asp His Arg

20 25 30

Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser Gly Ser Val

35 40 45

His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys

50 55 60

Ala Lys Glu Gly Gly Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn

65 70 75 80

Gly His Glu Pro Gln Gln Gly Lys Tyr Tyr Phe Glu Gly Arg Tyr Asp

85 90 95

Leu Val Lys Phe Ile Lys Leu Val His Gln Ala Gly Leu Tyr Val His

100 105 110

Leu Arg Val Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe

115 120 125

Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg Thr Asp Asn

130 135 140

Gly Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn

145 150 155 160

Met Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile

165 170 175

Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met Glu Trp Glu Leu Gly

180 185 190

Ala Pro Gly Lys Ser Tyr Ala Gln Trp Ala Ala Lys Met Ala Val Gly

195 200 205

Leu Asp Thr Gly Val Pro Trp Val Met Cys Lys Gln Asp Asp Ala Pro

210 215 220

Asp Pro Ile Ile Asn Ala Cys Asn Gly Phe Tyr Cys Asp Tyr Phe Ser

225 230 235 240

Pro Asn Lys Ala Tyr Lys Pro Lys Ile Trp Thr Glu Ala Trp Thr Ala
245 250 255

Trp Phe Thr Gly Phe Gly Asn Pro Val Pro Tyr Arg Pro Ala Glu Asp
260 265 270

Leu Ala Phe Ser Val Ala Lys Phe Ile Gln Lys Gly Gly Ser Phe Ile
275 280 285

Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr Ala Gly
290 295 300

Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu
305 310 315 320

Tyr Gly Leu Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His
325 330 335

Arg Ala Ile Lys Leu Cys Glu Pro Ala Leu Val Ser Gly Asp Pro Ala
340 345 350

Val Thr Ala Leu Gly His Gln Gln Glu Ala His Val Phe Arg Ser Lys
355 360 365

Ala Gly Ser Cys Ala Ala Phe Leu Ala Asn Tyr Asp Gln His Ser Phe
370 375 380

Ala Thr Val Ser Phe Ala Asn Arg His Tyr Asn Leu Pro Pro Trp Ser
385 390 395 400

Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Phe Asn Thr Ala Arg
405 410 415

Ile Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly
420 425 430

Leu Pro Trp Gln Ser Phe Asn Glu Glu Thr Ser Ser Tyr Glu Asp Ser
435 440 445

Ser Phe Thr Val Val Gly Leu Leu Glu Gln Ile Asn Thr Thr Arg Asp
450 455 460

Val Ser Asp Tyr Leu Trp Tyr Ser Thr Asp Val Lys Ile Asp Ser Arg
465 470 475 480

Glu Lys Phe Leu Arg Gly Gly Lys Trp Pro Trp Leu Thr Ile Met Ser
485 490 495

Ala Gly His Ala Leu His Val Phe Val Asn Gly Gln Leu Ala Gly Thr
500 505 510

Ala Tyr Gly Ser Leu Glu Lys Pro Lys Leu Thr Phe Ser Lys Ala Val
515 520 525

Asn Leu Arg Ala Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val
530 535 540

Gly Leu Pro Asn Ile Gly Pro His Phe Glu Thr Trp Asn Ala Gly Val
545 550 555 560

Leu Gly Pro Val Ser Leu Thr Gly Leu Asp Glu Gly Lys Arg Asp Leu
565 570 575

Thr Trp Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu
580 585 590

Ser Leu His Ser Leu Ser Gly Ser Ser Ser Val Glu Trp Val Glu Gly
595 600 605

Ser Leu Val Ala Gln Arg Gln Pro Leu Thr Trp Tyr Lys Ser Thr Phe
610 615 620

Asn Ala Pro Ala Gly Asn Asp Pro Leu Ala Leu Asp Leu Asn Thr Met
625 630 635 640

Gly Lys Gly Gln Val Trp Ile Asn Gly Gln Ser Leu Gly Arg Tyr Trp
645 650 655

Pro Gly Tyr Lys Ala Ser Gly Asn Cys Gly Ala Cys Asn Tyr Ala Gly
660 665 670

Trp Phe Asn Glu Lys Lys Cys Leu Ser Asn Cys Gly Glu Ala Ser Gln
675 680 685

Arg Trp Tyr His Val Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu
690 695 700

Leu Val Leu Phe Glu Glu Trp Gly Gly Glu Pro His Gly Ile Ser Leu
705 710 715 720

Val Lys Arg Glu Val Ala Ser Val Cys Ala Asp Ile Asn Glu Trp Gln

725 730 735

Pro Gln Leu Val Asn Trp Gln Met Gln Ala Ser Gly Lys Val Asp Lys
740 745 750

Pro Leu Arg Pro Lys Ala His Leu Ser Cys Ala Ser Gly Gln Lys Ile
755 760 765

Thr Ser Ile Lys Phe Ala Ser Phe Gly Thr Pro Gln Gly Val Cys Gly
770 775 780

Ser Phe Arg Glu Gly Ser Cys His Ala Phe His Ser Tyr Asp Ala Phe
785 790 795 800

Glu Arg Tyr Cys Ile Gly Gln Asn Ser Cys Ser Val Pro Val Thr Pro
805 810 815

Glu Ile Phe Gly Gly Asp Pro Cys Pro His Val Met Lys Lys Leu Ser
820 825 830

Val Glu Val Ile Cys Ser
835

<210> 11

<211> 724

<212> PRT

<213> Lycopersicon esculentum

<400> 11

Met Leu Arg Thr Asn Val Leu Leu Leu Val Ile Cys Leu Leu Asp
1 5 10 15

Phe Phe Ser Ser Val Lys Ala Ser Val Ser Tyr Asp Asp Arg Ala Ile
20 25 30

Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile His Tyr
35 40 45

Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys
50 55 60

Asp Gly Gly Leu Asp Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His
65 70 75 80

Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg Tyr Asp Leu Val

85 90 95
Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg
100 105 110

Ile Gly Pro Tyr Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val
115 120 125

Trp Leu Lys Tyr Val Pro Gly Met Glu Phe Arg Thr Asn Asn Gln Pro
130 135 140

Phe Lys Val Ala Met Gln Gly Phe Val Gln Lys Ile Val Asn Met Met
145 150 155 160

Lys Ser Glu Asn Leu Phe Glu Ser Gln Gly Gly Pro Ile Ile Met Ala
165 170 175

Gln Ile Glu Asn Glu Tyr Gly Pro Val Glu Trp Glu Ile Gly Ala Pro
180 185 190

Gly Lys Ala Tyr Thr Lys Trp Ala Ala Gln Met Ala Val Gly Leu Lys
195 200 205

Thr Gly Val Pro Trp Ile Met Cys Lys Gln Glu Asp Ala Pro Asp Pro
210 215 220

Val Ile Asp Thr Cys Asn Gly Phe Tyr Cys Glu Gly Phe Arg Pro Asn
225 230 235 240

Lys Pro Tyr Lys Pro Lys Met Trp Thr Glu Val Trp Thr Gly Trp Tyr
245 250 255

Thr Lys Phe Gly Gly Pro Ile Pro Gln Arg Pro Ala Glu Asp Ile Ala
260 265 270

Phe Ser Val Ala Arg Phe Val Gln Asn Asn Gly Ser Phe Phe Asn Tyr
275 280 285

Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr Ser Ser Gly Leu
290 295 300

Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly
305 310 315 320

Leu Leu Asn Glu Pro Lys Tyr Gly His Leu Arg Asp Leu His Lys Ala
325 330 335

Ile Lys Leu Ser Glu Pro Ala Leu Val Ser Ser Tyr Ala Ala Val Thr
340 345 350

Ser Leu Gly Ser Asn Gln Glu Ala His Val Tyr Arg Ser Lys Ser Gly
355 360 365

Ala Cys Ala Ala Phe Leu Ser Asn Tyr Asp Ser Arg Tyr Ser Val Lys
370 375 380

Val Thr Phe Gln Asn Arg Pro Tyr Asn Leu Pro Pro Trp Ser Ile Ser
385 390 395 400

Ile Leu Pro Asp Cys Lys Thr Ala Val Tyr Asn Thr Ala Gln Val Asn
405 410 415

Ser Gln Ser Ser Ser Ile Lys Met Thr Pro Ala Gly Gly Gly Leu Ser
420 425 430

Trp Gln Ser Tyr Asn Glu Glu Thr Pro Thr Ala Asp Asp Ser Asp Thr
435 440 445

Leu Thr Ala Asn Gly Leu Trp Glu Gln Lys Asn Val Thr Arg Asp Ser
450 455 460

Ser Asp Tyr Leu Trp Tyr Met Thr Asn Val Asn Ile Ala Ser Asn Glu
465 470 475 480

Gly Phe Leu Lys Asn Gly Lys Asp Pro Tyr Leu Thr Val Met Ser Ala
485 490 495

Gly His Val Leu His Val Phe Val Asn Gly Lys Leu Ser Gly Thr Val
500 505 510

Tyr Gly Thr Leu Asp Asn Pro Lys Leu Thr Tyr Ser Gly Asn Val Lys
515 520 525

Leu Arg Ala Gly Ile Asn Lys Ile Ser Leu Leu Ser Val Ser Val Gly
530 535 540

Leu Pro Asn Val Gly Val His Tyr Asp Thr Trp Asn Ala Gly Val Leu
545 550 555 560

Gly Pro Val Thr Leu Ser Gly Leu Asn Glu Gly Ser Arg Asn Leu Ala
565 570 575

Lys Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser

580 585 590

Leu His Ser Leu Ser Gly Ser Ser Ser Val Glu Trp Val Arg Gly Ser
595 600 605

Leu Met Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Ala Thr Phe Asn
610 615 620

Ala Pro Gly Gly Asn Asp Pro Leu Ala Leu Asp Met Ala Ser Met Gly
625 630 635 640

Lys Gly Gln Ile Trp Ile Asn Gly Glu Gly Val Gly Arg His Trp Pro
645 650 655

Gly Tyr Ile Ala Gln Gly Asp Cys Ser Lys Cys Ser Tyr Ala Gly Thr
660 665 670

Phe Asn Glu Lys Lys Cys Gln Thr Asn Cys Gly Gln Pro Ser Gln Arg
675 680 685

Trp Tyr His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn Leu Leu
690 695 700

Val Val Phe Glu Glu Trp Gly Gly Asn Pro Thr Gly Ile Ser Leu Val
705 710 715 720

Arg Arg Ser Arg

<210> 12

<211> 251

<212> PRT

<213> Lycopersicon esculentum

<400> 12

Ile Gln Thr Tyr Val Phe Trp Asn Leu His Glu Pro Val Arg Asn Gln
1 5 10 15

Tyr Asp Phe Glu Gly Arg Lys Asp Leu Ile Asn Phe Val Lys Leu Val
20 25 30

Glu Arg Ala Gly Leu Phe Val His Ile Arg Ile Gly Pro Tyr Val Cys
35 40 45

Ala Glu Trp Asn Tyr Gly Gly Phe Pro Leu Trp Leu His Phe Ile Pro

50 55 60

Gly Ile Glu Phe Arg Thr Asp Asn Glu Pro Phe Lys Ala Glu Met Lys
65 70 75 80

Arg Phe Thr Ala Lys Ile Val Asp Met Ile Lys Gln Glu Asn Leu Tyr
85 90 95

Ala Ser Gln Gly Gly Pro Val Ile Leu Ser Gln Ile Glu Asn Glu Tyr
100 105 110

Gly Asn Gly Asp Ile Glu Ser Arg Tyr Gly Pro Arg Ala Lys Pro Tyr
115 120 125

Val Asn Trp Ala Ala Ser Met Ala Thr Ser Leu Asn Thr Gly Val Pro
130 135 140

Trp Val Met Cys Gln Gln Pro Asp Ala Pro Pro Ser Val Ile Asn Thr
145 150 155 160

Cys Asn Gly Phe Tyr Cys Asp Gln Phe Lys Gln Asn Ser Asp Lys Thr
165 170 175

Pro Lys Met Trp Thr Glu Asn Trp Thr Gly Trp Phe Leu Ser Phe Gly
180 185 190

Gly Phe Val Pro Tyr Arg Pro Val Glu Asp Ile Ala Phe Ala Val Ala
195 200 205

Arg Phe Phe Gln Arg Gly Gly Thr Phe Gln Asn Tyr Tyr Met Tyr His
210 215 220

Gly Gly Thr Asn Phe Gly Arg Thr Ser Gly Gly Pro Phe Ile Ala Thr
225 230 235 240

Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr
245 250

<210> 13

<211> 249

<212> PRT

<213> Lycopersicon esculentum

<400> 13

Ile Gln Thr Tyr Val Phe Trp Asn Val His Glu Pro Ser Pro Gly Asn

1 5 10 15

Tyr Asn Phe Glu Gly Arg Tyr Asp Leu Val Arg Phe Val Lys Thr Ile
20 25 30

Gln Lys Ala Gly Leu Tyr Ala His Leu Arg Ile Gly Pro Tyr Val Cys
35 40 45

Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro
50 55 60

Gly Ile Ser Phe Arg Ala Asp Asn Glu Pro Phe Lys Asn Ala Met Lys
65 70 75 80

Gly Tyr Ala Glu Lys Ile Val Asn Leu Met Lys Ile Ile Ile Phe Ser
85 90 95

Ser Leu Arg Val Val Gln Ser Tyr Ser His Arg Leu Arg Met Ser Met
100 105 110

Gly Leu Lys Pro Arg Tyr Leu Glu His Arg Asp Ile Ser Ile Gln His
115 120 125

Gly Leu Gln Ile Trp Gln Leu Asp Leu Asn Thr Gly Val Pro Trp Val
130 135 140

Met Cys Lys Glu Glu Asp Ala Pro Asp Pro Val Ile Asn Thr Cys Asn
145 150 155 160

Gly Phe Tyr Cys Asp Asn Phe Phe Pro Asn Lys Pro Tyr Lys Pro Ala
165 170 175

Ile Trp Thr Glu Ala Trp Ser Gly Trp Phe Ser Glu Phe Gly Gly Pro
180 185 190

Leu His Gln Arg Pro Val Gln Asp Leu Ala Phe Ala Val Ala Gln Phe
195 200 205

Ile Gln Arg Gly Gly Ser Phe Val Asn Tyr Tyr Met Tyr His Gly Gly
210 215 220

Thr Asn Phe Gly Arg Thr Ala Gly Gly Pro Phe Ile Thr Thr Ser Tyr
225 230 235 240

Asp Tyr Asp Ala Pro Leu Asp Glu Tyr
245

<210> 14

<211> 870

<212> PRT

<213> Lycopersicon esculentum

<400> 14

Met Asn Thr Met Ser Cys Leu Ser Ser Asn Phe Lys Phe Val Phe Leu

1 5 10 15

Ala Ser Thr Val Ile Trp Met Thr Val Met Ser Ser Ser Leu Ala Ala

20 25 30

Val Asp Ala Ser Asn Val Thr Thr Ile Gly Thr Asp Ser Val Thr Tyr

35 40 45

Asp Arg Arg Ser Leu Ile Ile Asn Gly Gln Arg Lys Leu Leu Ile Ser

50 55 60

Ala Ser Ile His Tyr Pro Arg Ser Val Pro Ala Met Trp Pro Gly Leu

65 70 75 80

Val Arg Leu Ala Lys Glu Gly Gly Val Asp Val Ile Glu Thr Tyr Val

85 90 95

Phe Trp Asn Gly His Glu Pro Ser Pro Gly Asn Tyr Tyr Phe Gly Gly

100 105 110

Arg Phe Asp Leu Val Lys Phe Cys Lys Ile Ile Gln Gln Ala Gly Met

115 120 125

Tyr Met Ile Leu Arg Ile Gly Pro Phe Val Ala Ala Glu Trp Asn Phe

130 135 140

Gly Gly Leu Pro Val Trp Leu His Tyr Val Pro Gly Thr Thr Phe Arg

145 150 155 160

Thr Asp Ser Glu Pro Phe Lys Tyr His Met Gln Lys Phe Met Thr Tyr

165 170 175

Thr Val Asn Leu Met Lys Arg Glu Arg Leu Phe Ala Ser Gln Gly Gly

180 185 190

Pro Ile Ile Leu Ser Gln Val Glu Asn Glu Tyr Gly Tyr Tyr Glu Asn

195 200 205

Ala Tyr Gly Glu Gly Gly Lys Arg Tyr Ala Leu Trp Ala Ala Lys Met
210 215 220

Ala Leu Ser Gln Asn Thr Gly Val Pro Trp Ile Met Cys Gln Gln Tyr
225 230 235 240

Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn Ser Phe Tyr Cys Asp
245 250 255

Gln Phe Lys Pro Ile Ser Pro Asn Lys Pro Lys Ile Trp Thr Glu Asn
260 265 270

Trp Pro Gly Trp Phe Lys Thr Phe Gly Ala Arg Asp Pro His Arg Pro
275 280 285

Ala Glu Asp Val Ala Tyr Ser Val Ala Arg Phe Phe Gln Lys Gly Gly
290 295 300

Ser Val Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg
305 310 315 320

Thr Ala Gly Gly Pro Phe Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro
325 330 335

Ile Asp Glu Tyr Gly Leu Pro Arg Phe Pro Lys Trp Gly His Leu Lys
340 345 350

Glu Leu His Lys Val Ile Lys Ser Cys Glu His Ala Leu Leu Asn Asn
355 360 365

Asp Pro Thr Leu Leu Ser Leu Gly Pro Leu Gln Glu Ala Asp Val Tyr
370 375 380

Glu Asp Ala Ser Gly Ala Cys Ala Ala Phe Leu Ala Asn Met Asp Asp
385 390 395 400

Lys Asn Asp Lys Val Val Gln Phe Arg His Val Ser Tyr His Leu Pro
405 410 415

Ala Trp Ser Val Ser Ile Leu Pro Asp Cys Lys Asn Val Ala Phe Asn
420 425 430

Thr Ala Lys Val Gly Cys Gln Thr Ser Ile Val Asn Met Ala Pro Ile
435 440 445

Asp Leu His Pro Thr Ala Ser Ser Pro Lys Arg Asp Ile Lys Ser Leu

450

455

460

Gln Trp Glu Val Phe Lys Glu Thr Ala Gly Val Trp Gly Val Ala Asp

465

470

475

480

Phe Thr Lys Asn Gly Phe Val Asp His Ile Asn Thr Thr Lys Asp Ala

485

490

495

Thr Asp Tyr Leu Trp Tyr Thr Thr Ser Ile Phe Val His Ala Glu Glu

500

505

510

Asp Phe Leu Arg Asn Arg Gly Thr Ala Met Leu Phe Val Glu Ser Lys

515

520

525

Gly His Ala Met His Val Phe Ile Asn Lys Lys Leu Gln Ala Ser Ala

530

535

540

Ser Gly Asn Gly Thr Val Pro Gln Phe Lys Phe Gly Thr Pro Ile Ala

545

550

555

560

Leu Lys Ala Gly Lys Asn Glu Ile Ser Leu Leu Ser Met Thr Val Gly

565

570

575

Leu Gln Thr Ala Gly Ala Phe Tyr Glu Trp Ile Gly Ala Gly Pro Thr

580

585

590

Ser Val Lys Val Ala Gly Phe Lys Thr Gly Thr Met Asp Leu Thr Ala

595

600

605

Ser Ala Trp Thr Tyr Lys Ile Gly Leu Gln Gly Glu His Leu Arg Ile

610

615

620

Gln Lys Ser Tyr Asn Leu Lys Ser Lys Ile Trp Ala Pro Thr Ser Gln

625

630

635

640

Pro Pro Lys Gln Gln Pro Leu Thr Trp Tyr Lys Ala Val Val Asp Ala

645

650

655

Pro Pro Gly Asn Glu Pro Val Ala Leu Asp Met Ile His Met Gly Lys

660

665

670

Gly Met Ala Trp Leu Asn Gly Gln Glu Ile Gly Arg Tyr Trp Pro Arg

675

680

685

Arg Thr Ser Lys Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly

690

695

700

Lys Phe Asn Pro Asp Lys Cys Val Thr Gly Cys Gly Gln Pro Thr Gln
705 710 715 720

Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val
725 730 735

Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe
740 745 750

Ser Met Arg Lys Val Ser Gly Ala Cys Gly His Leu Ser Val Asp His
755 760 765

Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu Asn Asp
770 775 780

Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile
785 790 795 800

Ser Ser Val Lys Phe Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly
805 810 815

Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser Ala Ala Leu Val
820 825 830

Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser
835 840 845

Ala Asn Phe Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala
850 855 860

Val Glu Val Asn Cys Ser
865 870